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EFFECTS OF MIGRATION ON VECTOR-BORNE DISEASES WITH FORWARD AND BACKWARD STAGE PROGRESSION

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Abstract. Is it possible to break the host-vector chain of transmission when there is an influx of infectious hosts into a naïve population and competent vector? To address this question, a class of vector-borne disease models with an arbitrary number of infectious stages that account for immigration of infective individuals is formulated. The proposed model accounts for forward and backward progression, capturing the mitigation and aggravation to and from any stages of the infection, respectively. The model has a rich dynamic, which depends on the patterns of infected immigrant influx into the host population and connectivity of the transfer between infectious classes. We provide conditions under which the answer of the initial question is positive.

1. **Introduction.** Vector-borne diseases represent a major public health problem around the world, cause over one million deaths, one billion cases each year [43], and more than half of the world's population is at risk [42]. They are typically associated with the tropics and subtropics where these diseases are endemic. However, recently these diseases have expanded their geographical distribution and have been reported in many temperate countries. For instance, Dengue and Chikungunya have been reported in France [12, 13, 29, 38], Italy [30, 31], and Portugal [41]. The CDC recently [8] reported that mosquito, tick, and flea bite borne diseases tripled in the United States from 2004 through 2016.

Many drivers are reported to be behind the geographic expansion of vector-borne diseases, including but not limited to trade, travel, climate change, urbanization and other social upheaval phenomena [20, 21, 32]. Particularly, immigration and migration have been pointed to be the leading drivers in the emergence of vector-borne diseases in temperate nations [2]. For instance, a term *Airport malaria* has been coined by [18]. Indeed, it describes a malaria infection that has resulted from the bite of an infected tropical anopheline mosquito by persons whose geographic history excludes exposure to this vector in its natural habitat [18]. Hereafter, we use the term "immigrants" to represent both endemic area borne individuals migrating into a "naïve" area as well as non-endemic area native individuals who acquired an *airport vector-borne disease* after a stint in an endemic area. Naturally, the latter term follows the definition of *Airport malaria*.

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Moreover, the existence of vector populations that are capable of transmitting several arboviruses in the US and western Europe has been widely documented. For instance, the vector *Aedes albopictus* also known as the Asian tiger mosquito, a vector competent of transmitting many arbovirus including Japanese encephalitis, West Nile, and yellow fever, Dengue, etc., to humans [26, 33], is well established in North America [3, 26, 33] and Europe [26].

Together, the increasing interconnectedness of the world brings an influx of viremic (latent or infectious) individuals and their epidemiological life-history into naive geographic areas or populations, and thereby infecting local competent vector populations. This could potentially create a chain reaction that could lead to an autochthonous transmission cycle of arboviruses and sporadic outbreaks of vector-borne diseases in these otherwise naive host populations. For instance, the presumed index case of Italy's 2007 Chikungunya outbreak was a man from India who developed symptoms while visiting relatives in one of the villages where the outbreak started [31]. Similarly, an estimated 475 cases of imported chikungunya are reported in mainland France [29] from November 2013 to June 2014, and these cases are reportedly traced back to travelers returning from the French Caribbean islands where chikungunya and Dengue are endemic [29]. The 2012 Portugal's Dengue outbreak was reported to be imported by a traveler from Venezuela [41]. It is therefore important the gauge the impacts of infected immigrants of the dynamics of vector-borne diseases.

Typically, modeling the dynamics of directly transmitted or vector-borne diseases have often been based on the assumption that the recruitment into the considered population is completely susceptible, and thereby sweeping the effects of global movement of individuals across the world at unprecedented levels under the rug.

To the best of our knowledge, Brauer and van den Driessche [6] were the to first propose a mathematical model that accounts for immigration that includes infected individuals using an SIS structure in an attempt to study HIV in prisons. Subsequently, McCluskey and van den Driessche [25] proposed a model studied with the same features where both immigration of latent and infective are considered, in the context tuberculosis. These two papers [6, 25] showed that there is no disease-free equilibrium and that the endemic equilibrium (EE) is globally asymptotically stable. Indeed, the model proposed in [6] is a two-dimensional, and the Poincaré-Bendixson theorem has been used to study the global stability of the EE. In [25], the authors considered model is an $SEIS$ model and a geometric approach [22, 23] is used to prove the global stability of the EE. Li et *al.* [15] generalized the before-mentioned models for staged-progression model – by considering a model with n infectious stages and a proportion p_i of the total influx is incorporated for each infectious class I_i. The models in the before-mentioned papers are all for directly transmitted diseases.

Recently, Tumwiine et *al.* [37] investigated the effects of infected immigrants using an $SIR - SI$ Ross-Macdonal's model in the context of malaria and showed that the disease persists in host and vector populations whenever the proportion of infected immigrants is non zero. However, their model does not account of immigration of latent individuals, a critical category as these pass the precautionary measures of screenings, if these were in place. Moreover, for many vector-borne diseases, hosts' infectious period is variable, and infectivity to the vector population is not homogeneous. Indeed, for Chikungunya, after the incubation period, the

infectious period consists of two main stages: an acute stage, followed by a long-lasting chronic and incapacitating arthralgia [34, 40]. Similarly, Chagas disease is a two-phased disease with a differential infectivity to the vector population [10]. Dengue [9] and tick-borne relapsing fever [19] have been reported to exhibit multiple stages of infection, with varying parasitemia, thereby leading to a heterogeneous infectivity to vectors. For directly transmitted diseases, stage-progression models have been studied in [1, 17, 14]. These investigations do not account for the influx of infected and infectious individual into the host population, nor do they consider the relapse phenomenon – or backward stage progression – for which an infectious host at an advanced stage could improve its infectious state to an earlier stage.

In this paper, we derive and investigate the global behavior of a system that captures the dynamics of a class of vector-borne models accounting for flux of infected individuals at different stages of infection. Of particular interest is the impact of the influx of infected individuals and transfer rates between infectious classes on the overall the dynamics of the model. The paper is organized as follows:

• We derive a class of vector-borne models with n stages of infection, for which there is a flux of infected and infectious immigrants at all of these infectious stages. The formulated model accounts also for the progression and amelioration during the infectious stages, from an arbitrary stage i to an arbitrary stage j. The transfer is considered a progression if $i > j$ and an amelioration if $i < j$ (Section 2).

• We completely study the dynamics of the proposed model (Section 3). It turns out that the model has a variety of dynamics, which depends on the patterns of the influx infected host into the population and the transfer rate matrix – that describes the amelioration and deterioration of hosts' infectivity level. Particularly, we show that, under certain conditions, it is possible to corral the infectious hosts only into the classes in which they are replenished and maintain the vector populations disease-free. A threshold $\mathcal{N}^2(p_0, \mathbf{p}, p_{n+1})$ plays a critical role for the existence of such steady-state.

• We provide the global dynamics of the model when there is no influx of infected individuals into the population, which surprisingly has not been done (Section 3.1). In this case, the model exhibits the threshold phenomenon – the basic reproduction number $\mathcal{R}_0^2$ determines the outcome of the disease both in host and vector population. It happens that $\mathcal{R}_0^2 := \mathcal{N}^2(0, \mathbf{0}, 0)$.

• Illustrations of the results and numerical simulations are carried out in Section 4.

2. **Formulation of the model.** We consider a disease whose evolution is captured by a host-vector interaction for which the host population is composed of susceptible, exposed, recovered and infectious of stage i ($1 \leq i \leq n$). These subpopulations are denoted respectively by S_h, E_h, R_h and I_i. The total host population is therefore $N_h = S_h + E_h + \sum_{i=1}^{n} I_i + R_h$. The vector population N_v is composed of susceptible, exposed, and infectious arthropods; denoted by S_v, E_v, and I_v, respectively.

The total host population is replenished through a constant recruitment, π_h, that includes birth and migratory influx of individuals. Of this constant recruitment, a proportion p_0, p_i ($i = 1, \ldots, n$) and p_{n+1} is latent, infectious at stage i and recovered, respectively. Thus, the total recruitment in the susceptible class is $\pi_h \left(1 - \sum_{i=0}^{n+1} p_i\right)$. Naturally, we assume that, for all i, $0 \leq p_i \leq 1$ and $0 \leq \sum_{i=0}^{n+1} p_i < 1$.

Susceptible hosts are infected at the rate $a\beta_{vh}\frac{I_v}{N_n}$, where a is the biting/landing rate and β_{vh} is the Host's infectiousness by arthropod per biting/landing. Vector's infection term is captured by $aS_v\frac{\sum_{i=1}^{n}\beta_i I_i}{N_h}$, where β_i is the vector's infectiousness by infected hosts of stage i. This accounts for the differential infectivity of vectors with respect to hosts' infectious stages.

Motivated by [15, 16, 24], we incorporate incremental and non-incremental amelioration and recrudescence in the infectivity at each stage of the host's infection. For instance, for models in [4, 10, 28], the transitions between infection stages are incremental, that is, always from stage i to $i+1$. However, with vector-borne diseases, a bite of infected arthropod to an already infected host, say at stage i, may increase this host's parasitemia, thereby catapulting its infectious class from stage i to any stage, say j, where $i \leq j \leq n$. To incorporate this phenomenon, we denote by γ_{ij}, the *per capita* rate at which the host progresses from stage i to stage j. Similarly, the increase of treatments (which decrease the parasiteamia in the blood-stream) of vector-borne diseases could alleviate the host's infection and therefore, its stage could change form i to k, where $1 \leq k \leq i$. We denote by δ_{ik} the *per capita* rate at which the host regresses from stage i to stage k, where $k \leq i$. These generalizations are illustrated in Figure 1.

In concert, the overall dynamics of the Host-Vector infection is given by:

$$
\begin{cases}
\dot{S}_h = \pi_h\left(1-\sum_{i=0}^{n+1}p_i\right) - a\,\beta_{vh}\,S_h\,\frac{I_v}{N_h} - \mu_h S_h \\
\dot{E}_h = p_0\pi_h + a\beta_{vh}\,S_h\,\frac{I_v}{N_h} - (\mu_h+\nu_h+\eta)E_h \\
\dot{I}_1 = p_1\pi_h + \nu_h E_h - (\mu_h+\eta_1)I_1 - I_1\sum_{j=2}^{n}\gamma_{1j} + \sum_{j=2}^{n}\delta_{j1}I_j \\
\dot{I}_2 = p_2\pi_h - (\mu_h+\eta_2)I_2 - I_2\left(\sum_{j=1,j<2}^{n}\delta_{2j} + \sum_{j=1,j>2}^{n}\gamma_{2j}\right) \\
\qquad\qquad + \left(\sum_{j=1,j>2}^{n}\delta_{j2}I_j + \sum_{j=1,j<2}^{n}\gamma_{j2}I_j\right) \\
\vdots \\
\dot{I}_i = p_i\pi_h - (\mu_h+\eta_i)I_i - I_i\left(\sum_{j=1,j<i}^{n}\delta_{ij} + \sum_{j=1,j>i}^{n}\gamma_{ij}\right) \\
\qquad\qquad + \left(\sum_{j=1,j>i}^{n}\delta_{ji}I_j + \sum_{j=1,j<i}^{n}\gamma_{ji}I_j\right) \\
\dot{I}_n = p_i\pi_h - (\mu_h+\eta_n)I_n - I_n\sum_{j=1}^{n-1}\gamma_{nj} + \sum_{j=1}^{n-1}\delta_{jn}I_j \\
\dot{R}_h = p_{n+1}\pi_h + \sum_{i=1}^{n}\eta_i I_i - \mu_h R \\
\dot{S}_v = \pi_v - aS_v\sum_{i=1}^{n}\frac{\beta_i I_i}{N_h} - (\mu_v+\delta_v)S_v \\
\dot{E}_v = aS_v\sum_{i=1}^{n}\frac{\beta_i I_i}{N_h} - (\mu_v+\nu_v+\delta_v)E_v \\
\dot{I}_v = \nu_v E_v - (\mu_v+\delta_v)I_v
\end{cases}
\tag{1}
$$

To ease the notations, let us denote by

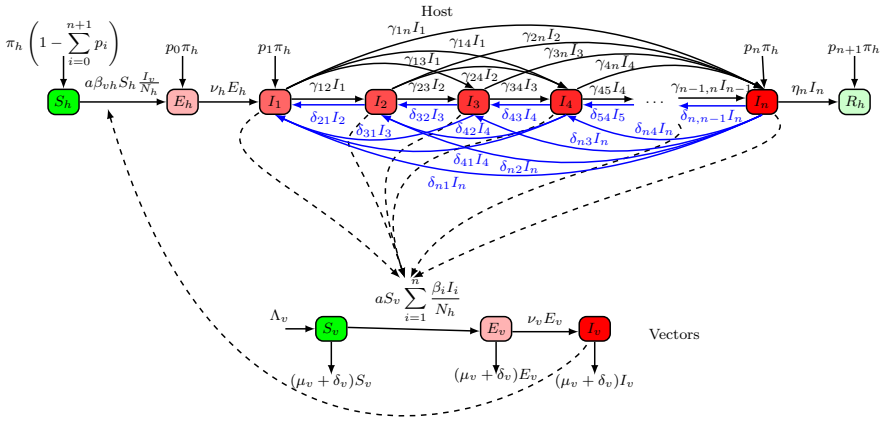


FIGURE 1. Flow diagram of Model 1. Note that, to unclutter the figure, we did not display the arrows that represent the recruitments for I_2, I_3 and I_4. Similarly, the arrows representing the death, μ_i, and recovery rates, η_i, in all host classes are not displayed.

$$m_{ij} = \begin{cases} \delta_{ji} & \text{if} \quad i < j, \\ 0 & \text{if} \quad i = j, \\ \gamma_{ji} & \text{if} \quad i > j, \end{cases}$$

and $\alpha_v = \mu_v + \nu_v + \delta_v$, $\alpha_1 = \mu_h + \eta_1 + \sum_{j=2}^{n} \gamma_{1j} = \mu_h + \eta_1 + \sum_{j=2}^{n} m_{j1}$ and for $i \geq 2$,

$$\begin{aligned} \alpha_i &= \mu_h + \eta_i + \left(\sum_{j=1, j<i}^{n} \delta_{ij} + \sum_{j=1, j>i}^{n} \gamma_{ij} \right) \\ &= \mu_h + \eta_i + \sum_{j=1}^{n} m_{ji}. \end{aligned}$$

The matrix $M = (m_{ij})_{1 \leq i,j \leq n}$ is the transfer matrix between Host's infectious classes and the parameters α_i represent the rates at which infected of stage i leave this stage. The total host population is asymptotically constant. Indeed, its evolution is given by $\dot{N}_h = \pi_h - \mu_h N_h$ and thus, it is straightforward to show that $\lim_{t \to \infty} N_h = \dfrac{\pi_h}{\mu_h}$. Moreover, the subsystem describing the dynamics of the host is triangular, and hence we can disregard the dynamics of the recovered host R_h. Hence, by abusively denoting $\lim_{t \to \infty} N_h$ again by N_h and using the theory of asymptotically autonomous systems for triangular systems [7, 39], System (1) could equivalently

be written in a compact form as follows:

$$\begin{cases} \dot{S}_h = \pi_h \left(1 - p_0 - \mathbb{1}^T \mathbf{p} - p_{n+1}\right) - a\,\beta_{vh}\,S_h\,\dfrac{I_v}{N_h} - \mu_h S_h \\ \dot{E}_h = p_0\pi_h + a\beta_{vh}\,S_h\,\dfrac{I_v}{N_h} - (\mu_h + \nu_h + \eta)E_h \\ \dot{\mathbf{I}}_h = \pi_h \mathbf{p} + \nu_h E_h e_1 - (\mathrm{diag}(\alpha) - M)\mathbf{I}_h \\ \dot{S}_v = \pi_v - a\dfrac{S_v}{N_h}\langle \boldsymbol{\beta} \,|\, \mathbf{I}_h \rangle - (\mu_v + \delta_v)S_v \\ \dot{E}_v = a\dfrac{S_v}{N_h}\langle \boldsymbol{\beta} \,|\, \mathbf{I}_h \rangle - (\mu_v + \nu_v + \delta_v)E_v \\ \dot{I}_v = \nu_v E_v - (\mu_v + \delta_v)I_v, \end{cases} \tag{2}$$

where $\mathbf{I}_h = (I_1, I_2, \ldots, I_n)^T$, $\boldsymbol{\beta} = (\beta_1, \beta_2, \ldots, \beta_n)^T$, $\mathbf{p} = (p_1, p_2, \ldots, p_n)^T$, and $M = G^T + D^T$ with $G = (\gamma_{ij})$ representing the progression matrix, or forward flow transition matrix while $D = (\delta_{ij})$ represents the amelioration matrix, or backward transition flow matrix. More precisely,

$$G = \begin{pmatrix} 0 & \gamma_{12} & \gamma_{13} & \ldots & \gamma_{1n} \\ 0 & 0 & \gamma_{23} & \ldots & \gamma_{2n} \\ \vdots & \vdots & \ddots & \ddots & \vdots \\ 0 & 0 & 0 & \ldots & \gamma_{n-1,n} \\ 0 & 0 & 0 & \ldots & 0 \end{pmatrix} \quad \text{and} \quad D = \begin{pmatrix} 0 & 0 & \ldots & 0 & 0 \\ \delta_{21} & 0 & \ldots & 0 & 0 \\ \vdots & \ddots & \ddots & \vdots & \vdots \\ \delta_{n-1,1} & \delta_{n-1,2} & \ldots & 0 & 0 \\ \delta_{n1} & \delta_{n2} & \ldots & \delta_{n,n-1} & 0 \end{pmatrix}. \tag{3}$$

The parameters of System (1) are described in Table 2. The flow chart capturing the infection process is represented in Fig. (1).

TABLE 1. Description of the parameters used in System (1).

Parameters	Description
π_h	Recruitment of the host
π_v	Recruitment of vectors
p_0	Proportion of latent immigrants
p_i	Proportion of infectious immigrants at stage i
a	Biting rate
μ_h	Host's natural death rate
$\beta_{v,h}$	Host's infectiousness by mosquitoes per biting
β_i	Vector's infectiousness by host at stage i per biting
ν_h	Host's rate at which the exposed individuals become infectious
η_i	Per capita recovery rate of an infected host at stage i
γ_{ij}	Host's per capita progression rate from stage i to j
δ_{ij}	Host's per capita regression rate from stage i to j
μ_v	Vectors' natural mortality rate
δ_v	Vectors' control-induced mortality rate
ν_v	Rate at which the exposed vectors become infectious

Model (2) follows an $SEI^nR - SEI$ structure. That is, of the host and vector populations dynamics follow an and SEI^nR and SEI types of model, respectively. The choices are make to capture some key features in modeling different vector-borne diseases. Indeed, many special cases could be obtained from our general framework to fit a particular arboviral disease. For instance, if $\nu_h \to \infty$, the Host's

dynamics will be an SI^nR model. An $SIR-SI$ model have been considered for malaria [37] and Dengue [11] while an SI^nR-SI model was deemed more suited for tick-borne relapsing fever [19, 28].

Model (2) generalizes other models proposed in the literature in the following five ways:

- If $D=\mathbf{0}_{n,n}$ and $\gamma_{ij}=0$ for all i,j, except when $j=i+1$, Model (2) consists of a class of staged progression vector-borne diseases models with an influx of infected individuals of each class into the considered population. In this case,
  - Model (2) extents the existing stage progression vector-borne models to incorporate a differential proportions of the overall recruitment in all infected classes. This allows us to gauge the impact of imported cases on the dynamics of vector-borne infections. When $\mathbf{p}=\mathbf{0}$, $p_0=0$, in Model (2), we obtain the model proposed and studied in [4]. Moreover, our model extends also [28], for which $\beta_i=\beta$, for all i and the recruitment constitutes of susceptible individuals only. Our model generalizes also [10], which considers Chagas disease model with two stages, namely acute and chronic phases.
  - Model (2) generalizes existing models that investigate staged-progression for directly transmitted infections for which influx of infected individuals are considered [15, 25] and [6], where no stages are considered in the latter.
  - Model (2) extends also the model in [37], where the authors considered a host-vector model $SIR-SI$ with infectious immigrants in investigating the effects of the latter on Malaria dynamics, by incorporating a latent class, n stages of infection in the host's dynamics and a differential infectivity of vectors with respect to host's infectious stages.
- If D and G are as defined in (3), our model extends [4, 6, 10, 15, 25, 28, 37] by incorporating forward (deterioration) and backward (amelioration) stage progression. Moreover, the progressions or regressions are not necessarily incremental.
- Model (2) extends the models considered in [15, 16, 24] to vector-borne disease models and the incorporation of influx of infected in each of the hosts' infectious classes.

Overall, Model (2) generalizes in some fashion or aspect models in [4, 6, 10, 15, 16, 25, 28, 37, 24].

Also, it is worthwhile to notice that our system could be seen as a class of models for vector-borne diseases that are vertically transmitted at each stage of the infection. That is, when off-springs are infected by mothers during pregnancy or delivery. Zika virus is a natural example of a vector-borne disease that is vertically transmitted [35].

The following result shows the solutions of Model (2) are positive and remain bounded at all times, thereby making the model biologically grounded.

Lemma 2.1. *The set*

$$\Omega=\left\{(S_h,E_h,\mathbf{I}_h,S_v,E_v,I_v)\in\mathbb{R}^{n+5}\ \middle|\ S_h+E_h+\mathbb{1}^T\mathbf{I}_h\le N_h:=\frac{\pi_h}{\mu_h},\right.$$
$$\left.S_v+E_v+I_v\le N_v:=\frac{\pi_v}{\mu_v+\delta_v}\right\}$$

is a compact positively invariant for System (2).

In the next section, we investigate the steady states solutions of Model (2) and their asymptotic behavior.

3. Global stability analysis.

The next theorem establishes the existence of endemic equilibria of System (2) and provides conditions under which they may exist. Following Thieme [36], we use the nomenclature *strongly* endemic equilibrium if all of its components are positive and *weakly* endemic equilibrium, if at least one of the infected component is positive. Naturally, we start with the assumption that $\mathbf{p} \neq \mathbf{0}_{\mathbb{R}^n}$. The case $\mathbf{p} = \mathbf{0}_{\mathbb{R}^n}$ is dealt in Section 3.1.

Theorem 3.1. *The equilibria of System (2) are as follows:*

1. *If $\boldsymbol{\beta} = 0$, a unique weakly endemic equilibrium $(\bar{S}_h, \bar{E}_h, \bar{\mathbf{I}}_h, \bar{S}_v, 0, 0)$ exists.*
2. *If $\boldsymbol{\beta} \neq 0$ and $p_0 \neq 0$, it exists a unique strongly endemic equilibrium $(S_h^*, E_h^*, \mathbf{I}_h^*, S_v^*, E_v^*, I_v^*)$.*
3. *If $\boldsymbol{\beta}$ and $\mathbf{p}$ are such that $\left\langle \boldsymbol{\beta} \,\middle|\, (diag(\alpha) - M)^{-1}\mathbf{p} \right\rangle \neq 0$, a unique strongly endemic equilibrium $(S_h^\sharp, E_h^\sharp, \mathbf{I}_h^\sharp, S_v^\sharp, E_v^\sharp, I_v^\sharp)$ exists.*
4. *If Item 1, Item 2 and Item 3 are not satisfied, then a threshold $\mathcal{N}_0^2(p_0, \mathbf{p}, p_{n+1})$, defined by*

$$\mathcal{N}_0^2(p, \mathbf{p}, p_{n+1}) = \frac{a^2 \beta_{vh} \nu_v \nu_h N_v}{\alpha_v(\mu_v + \delta_v)\alpha_h \mu_h} \frac{\pi_h \left(1 - p_0 - \mathbb{1}^T \mathbf{p} - p_{n+1}\right)}{N_h^2} \left\langle \boldsymbol{\beta} \,\middle|\, (diag(\alpha) - M)^{-1} e_1 \right\rangle,$$

exists and for which

- *If $\mathcal{N}_0^2(p_0, \mathbf{p}, p_{n+1}) \leq 1$, a unique weakly endemic equilibrium $(S_h^\diamond, 0, \mathbf{I}_h^\diamond, S_v^0, 0, 0)$ where $\mathbf{I}_h^\diamond > 0$ exists.*
- *If $\mathcal{N}_0^2(p_0, \mathbf{p}, p_{n+1}) > 1$, a unique strongly endemic equilibrium $(\tilde{S}_h, \tilde{E}_h, \tilde{\mathbf{I}}_h, \tilde{S}_v, \tilde{E}_v, \tilde{I}_v)$ exists.*

Proof. An equilibrium $(S_h^*, E_h^*, I_h^*, \ldots, I_n^*, S_v^*, E_v^*, I_v^*)$ for Model (2) satisfies the following relations.

$$\begin{cases} \Lambda_h = a\,\beta_{vh}\, S_h^* \dfrac{I_v^*}{N_h} + \mu_h S_h^* \\ (\mu_h + \nu_h + \eta) E_h^* = p_0 \pi_h + \beta_{vh}\, S_h^* \dfrac{I_v^*}{N_h} \\ (\mathrm{diag}(\alpha) - M)\mathbf{I}_h^* = \pi_h \mathbf{p} + \nu_h E_h^* e_1 \\ \pi_v = a \dfrac{S_v^*}{N_h} \left\langle \boldsymbol{\beta} \,\middle|\, \mathbf{I}_h^* \right\rangle + (\mu_v + \delta_v) S_v^* \\ (\mu_v + \nu_v + \delta_v) E_v^* = a \dfrac{S_v^*}{N_h} \left\langle \boldsymbol{\beta} \,\middle|\, \mathbf{I}_h^* \right\rangle \\ (\mu_v + \delta_v) I_v^* = \nu_v E_v^*, \end{cases} \tag{4}$$

where $\Lambda_h = \pi_h \left(1 - p_0 - \mathbb{1}^t \mathbf{p} - p_{n+1}\right)$. Using these relationship and $N_v = S_v - E_v - I_v$, one could express I_v^* in terms of $\mathbf{I}_h^*$, as follows:

$$I_v^* \left(\mu_v + \delta_v + \frac{a}{N_h} \left\langle \boldsymbol{\beta} \,\middle|\, \mathbf{I}_h^* \right\rangle \right) = \frac{a\nu_v}{(\mu_v + \nu_v + \delta_v)} \frac{N_v}{N_h} \left\langle \boldsymbol{\beta} \,\middle|\, \mathbf{I}_h^* \right\rangle. \tag{5}$$

Moreover, the first equation of (4) leads to:

$$S_h^* = \frac{\Lambda_h N_h}{\mu_h N_h + a\beta_{vh} I_v^*} > 0.$$

Furthermore, since the matrix $\mathrm{diag}(\alpha) - M$ is strictly diagonally dominant and thus invertible, we obtain:

$$\mathbf{I}_h^* = \pi_h(\mathrm{diag}(\alpha) - M)^{-1}\mathbf{p} + \nu_h E_h^*(\mathrm{diag}(\alpha) - M)^{-1}e_1,$$

and

$$E_h^* = \frac{1}{(\mu_h + \nu_h + \eta)}\left(p_0\pi_h + \frac{\Lambda_h a\,\beta_{vh} I_v^*}{\mu_h N_h + a\beta_{vh} I_v^*}\right).$$

Therefore, $\mathbf{I}_h^*$ could be written as:

$$\mathbf{I}_h^* = \pi_h(\mathrm{diag}(\alpha) - M)^{-1}\mathbf{p} + \frac{\nu_h}{(\mu_h + \nu_h + \eta)}\left(p_0\pi_h + \frac{\Lambda_h a\,\beta_{vh} I_v^*}{\mu_h N_h + a\beta_{vh} I_v^*}\right)(\mathrm{diag}(\alpha) - M)^{-1}e_1. \tag{6}$$

The relation (6) is key for the remaining of the proof, as we will use it to compute $\langle \boldsymbol{\beta} \,|\, \mathbf{I}_h^* \rangle$ and obtain a quadratic equation in I_v^* using Equation (5). The latter equation leads to:

$$\begin{aligned} 0 = I_v^* \Bigg(& \mu_v + \delta_v + \frac{a}{N_h}\langle \boldsymbol{\beta} \,|\, \pi_h(\mathrm{diag}(\alpha) - M)^{-1}\mathbf{p}\rangle + \\ & + \frac{a}{N_h}\frac{\nu_h}{(\mu_h + \nu_h + \eta)}\left(p_0\pi_h + \frac{\Lambda_h a\,\beta_{vh} I_v^*}{\mu_h N_h + a\beta_{vh} I_v^*}\right)\langle \boldsymbol{\beta} \,|(\mathrm{diag}(\alpha) - M)^{-1}e_1\rangle\Bigg) - \\ & \frac{a\nu_v}{(\mu_v + \nu_v + \delta_v)}\frac{N_v}{N_h}\langle \boldsymbol{\beta} \,|\, \pi_h(\mathrm{diag}(\alpha) - M)^{-1}\mathbf{p}\rangle - \\ & \frac{\nu_h N_v}{(\mu_h + \nu_h + \eta)N_h}\left(p_0\pi_h + \frac{\Lambda_h a\,\beta_{vh} I_v^*}{\mu_h N_h + a\beta_{vh} I_v^*}\right)\frac{a\nu_v}{(\mu_v + \nu_v + \delta_v)}\langle \boldsymbol{\beta} \,|\, (\mathrm{diag}(\alpha) - M)^{-1}e_1\rangle \end{aligned} \tag{7}$$

After some rearrangement, Equation (7) could be written as

$$AI_v^{*2} + BI_v^* + C = 0, \tag{8}$$

where

$$\begin{aligned} A = a\beta_{vh}\Bigg[& \mu_v + \delta_v + \frac{a}{N_h}\langle \boldsymbol{\beta} \,|\, \pi_h(\mathrm{diag}(\alpha) - M)^{-1}\mathbf{p}\rangle + \\ & + \frac{a}{N_h}\frac{\nu_h}{(\mu_h + \nu_h + \eta)}\left(p_0\pi_h + \Lambda_h\right)\langle \boldsymbol{\beta} \,|(\mathrm{diag}(\alpha) - M)^{-1}e_1\rangle\Bigg] \\ & > 0, \end{aligned}$$

$$\begin{aligned} B = {} & (\mu_v + \delta_v)\mu_n N_h + \frac{a}{N_h}\pi_h\langle \boldsymbol{\beta} \,|\, (\mathrm{diag}(\alpha) - M)^{-1}\mathbf{p}\rangle\mu_h N_h \\ & + \frac{a}{N_h}\frac{\nu_h}{(\mu_h + \nu_h + \eta)}p_0\pi_h\langle \boldsymbol{\beta} \,|(\mathrm{diag}(\alpha) - M)^{-1}e_1\rangle\mu_n N_h \\ & - \frac{a^2\beta_{vh}\nu_v}{(\mu_v + \nu_v + \delta_v)}\frac{N_v}{N_h}\pi_h\langle \boldsymbol{\beta} \,|\, (\mathrm{diag}(\alpha) - M)^{-1}\mathbf{p}\rangle \\ & - \frac{a^2\beta_{vh}\nu_v\nu_h}{(\mu_v + \nu_v + \delta_v)(\mu_h + \nu_h + \eta)}\frac{N_v}{N_h}p_0\pi_h\langle \boldsymbol{\beta} \,|\, (\mathrm{diag}(\alpha) - M)^{-1}e_1\rangle \\ & - \frac{a^2\beta_{vh}\nu_v\nu_h}{(\mu_v + \nu_v + \delta_v)(\mu_h + \nu_h + \eta)}\frac{N_v}{N_h}\Lambda_h\langle \boldsymbol{\beta} \,|\, (\mathrm{diag}(\alpha) - M)^{-1}e_1\rangle, \end{aligned}$$

and

$$C = -\frac{a\nu_v}{(\mu_v+\nu_v+\delta_v)}\frac{N_v}{N_h}\pi_h\mu_h N_h\left\langle \boldsymbol{\beta}\,\middle|\,\pi_h(\mathrm{diag}(\alpha)-M)^{-1}\mathbf{p}\right\rangle$$
$$-\frac{a\nu_v N_v}{(\mu_v+\nu_v+\delta_v)}\frac{N_v}{N_h}\frac{\nu_h\mu_h N_h}{(\mu_h+\nu_h+\eta)}p_0\pi_h\left\langle \boldsymbol{\beta}\,\middle|\,(\mathrm{diag}(\alpha)-M)^{-1}e_1\right\rangle.$$

Now, we investigate cases for which Equation (7) has non-negative solutions.

• If $\boldsymbol{\beta}=0$, then $C=0$ and $B=(\mu_v+\delta_v)\mu_n N_h>0$. Hence, $I_v^*=0$ is the unique solution of the quadratic equation. Thus, the unique equilibrium for System (2) is $(\bar{S}_h,\bar{E}_h,\bar{\mathbf{I}}_h,\bar{S}_v,0,0)$, where $\bar{S}_h=\frac{\Lambda_h}{\mu_h}$, $\bar{E}_h=\frac{p\pi_h}{(\mu_h+\nu_h+\eta)}$, $\bar{\mathbf{I}}_h^*=\pi_h(\mathrm{diag}(\alpha)-M)^{-1}\mathbf{p}+\frac{\nu_h p\pi_h}{(\mu_h+\nu_h+\eta)}(\mathrm{diag}(\alpha)-M)^{-1}e_1$, and $\bar{S}_v=\frac{\Lambda_v}{\mu_v+\delta_v}$. This proves Item 1.

• If $\boldsymbol{\beta}\neq 0$ and $p_0\neq 0$, then $C<0$ and therefore Equation (8) has a unique solution such that $I_v^*>0$. Thus, from Equation (6), System (4), and using the fact that $(\mathrm{diag}(\alpha)-M)^{-1}e_1\gg 0$, we deduce Item 2.

• If $\boldsymbol{\beta}$ and $\mathbf{p}$ are such that $\left\langle \boldsymbol{\beta}\,\middle|\,(\mathrm{diag}(\alpha)-M)^{-1}\mathbf{p}\right\rangle\neq 0$, then we also have $C<0$; that is, it exists a unique $I_v^\sharp>0$ of Equation (8). As in the previous point, this leads to Item 3.

• If the conditions of Item 1, Item 2 and Item 3 are not satisfied; that is, if $\boldsymbol{\beta}\neq 0$, $p_0=0$ and $\mathbf{p}$ is such that $\left\langle \boldsymbol{\beta}\,\middle|\,(\mathrm{diag}(\alpha)-M)^{-1}\mathbf{p}\right\rangle=0$. In this case, $C=0$ and B could be written as:

$$\begin{aligned}B&=(\mu_v+\delta_v)\mu_h N_h\\&\quad-\frac{a^2\beta_{vh}\nu_v\nu_h}{(\mu_v+\nu_v+\delta_v)(\mu_h+\nu_h+\eta)}\frac{N_v}{N_h}\Lambda_h\left\langle \boldsymbol{\beta}\,\middle|\,(\mathrm{diag}(\alpha)-M)^{-1}e_1\right\rangle\\&=(\mu_v+\delta_v)\mu_h N_h\left[1-\right.\\&\left.\frac{a^2\beta_{vh}\nu_v\nu_h}{(\mu_v+\nu_v+\delta_v)(\mu_v+\delta_v)(\mu_h+\nu_h+\eta)\mu_h}\frac{N_v}{N_h}\frac{\Lambda_h}{N_h}\left\langle \boldsymbol{\beta}\,\middle|\,(\mathrm{diag}(\alpha)-M)^{-1}e_1\right\rangle\right]\\&=(\mu_v+\delta_v)\mu_h N_h\left(1-\mathcal{N}_0^2(p_0,\mathbf{p},p_{n+1})\right).\end{aligned}$$

Thus, it follows that if $\mathcal{N}_0^2(p_0,\mathbf{p},p_{n+1})\leq 1$, then $B\geq 0$, leading to $I_v^*=0$ and $\mathbf{I}_h^*=\pi_h(\mathrm{diag}(\alpha)-M)^{-1}\mathbf{p}>\mathbf{0}_{\mathbb{R}^n}$. If $\mathcal{N}_0^2(p_0,\mathbf{p},p_{n+1})>1$, then $B<0$ and therefore $I_v^*>0$, leading to a strongly positive equilibrium. □

The different scenarios presented in Theorem 3.1 have intuitive interpretations as follows:

- The condition of Item 1 – $\boldsymbol{\beta}=\mathbf{0}_{\mathbb{R}^n}$ – means that the local vector population is not competent to acquire the infectious pathogen. And so, even if there is an influx of infected or infectious hosts into the naive population, the vector population stays disease free and there will be infected or infectious hosts in population, due to the continuous influx of latent or infectious hosts. Thus, the system reaches an weakly endemic equilibrium.
- The condition of Item 2 – $\boldsymbol{\beta}\neq 0$ and $p_0\neq 0$ – means that if the vector is competent in acquiring the infectious agent, then the influx of latent individuals into the population is sufficient for the disease to persist within the host and vector populations. This condition leads to the existence of a strongly endemic equilibrium.
- The condition of Item 3 – $\boldsymbol{\beta}$ and $\mathbf{p}$ are such that $\left\langle \boldsymbol{\beta}\,\middle|\,(\mathrm{diag}(\alpha)-M)^{-1}\mathbf{p}\right\rangle\neq 0$ – states that if the patterns of the arthropod's competency to different stages of

the hosts' infectivity and those of the influx of infectious hosts' into the naive population and the transfer matrix M that describes the flow between the infectious classes, are such that the above condition is satisfied, the disease will persist in host and vector populations. This case include also the case where the set of indices of vector competency and the set of indices for infectious influx are disjoint. That is, the host in whichever infectious stage in which there is an influx of infectious hosts, will not able to transmit the pathogen to the vector population. In this particular case, the forward and backward transition patterns (from any stage to another) allow the infection to persist in the host and vector population.

- The condition of Item 4 – $p_0 = 0$, $\boldsymbol{\beta}$, $\mathbf{p}$ the transition matrix M are such that $\langle \boldsymbol{\beta} \,|\, (\mathrm{diag}(\alpha) - M)^{-1}\mathbf{p} \rangle = 0$ – means that there is no influx of latent hosts and that: a) there is an influx of infectious individuals only to a subset of stages and that the hosts in these stages are unable to infect the vectors and b.) the infectious hosts at these stages do not "ameliorate" or "deteriorate" their infectiosity to stages in the complement of the subset in which they belong. In this case the disease either persists in all hosts and vector population or dies out in the vector population and persists in host population only through migration, depending on whether the threshold $\mathcal{N}_0^2(p_0, \mathbf{p}, p_{n+1})$ is above or under unity, respectively.

The following two theorems establish the global stability analysis for the two types of endemic equilibria exhibited in Theorem 3.1. This gives a complete description of the global asymptotic behavior of System (2) whenever there is an influx of infected or infectious individuals into the population.

Theorem 3.2. *Let $(S_h^*, E_h^*, \mathbf{I}_h^*, S_v^*, E_v^*, I_v^*)$ be a strongly endemic equilibrium of Model (2). This equilibrium is globally asymptotically stable whenever it exists.*

Proof. Let consider the following Lyapunov function $\mathcal{V} = \mathcal{V}_h + \mathcal{V}_v$, where

$$\mathcal{V}_h = c_0 \int_{S_h^*}^{S_h} \left(1 - \frac{S_h^*}{x}\right) dx + c_0 \int_{E_h^*}^{E_h} \left(1 - \frac{E_h^*}{x}\right) dx + \sum_{i=1}^{n} c_i \int_{I_i^*}^{I_i} \left(1 - \frac{I_i^*}{x}\right) dx,$$

and,

$$\mathcal{V}_v = c_v \int_{S_v^*}^{S_v} \left(1 - \frac{S_v^*}{x}\right) dx + c_v \int_{E_v^*}^{E_v} \left(1 - \frac{E_v^*}{x}\right) dx + \frac{\mu_v + \nu_v + \delta_v}{\nu_v} c_v \int_{I_v^*}^{I_v} \left(1 - \frac{I_v^*}{x}\right) dx.$$

The coefficients $c = (c_1, c_2, \ldots, c_n)^T$ are positive to be determined later. The coefficient c_0 and c_v are related to c_1 as follows:

$$c_0 a \beta_{vh} S_h^* \frac{I_v^*}{N_h} = c_1 \nu_h E_h^* \quad \text{and} \quad c_v a S_v^* \frac{1}{N_h} = c_1 \frac{\nu_h E_h^*}{\sum_{i=1}^{n} \beta_i I_i^*}. \tag{9}$$

This function is definite positive. We want to prove that its derivative along the trajectories of System (2) is definite-negative. Throughout the proof, we will be using the component-wise endemic relations (4). That is,

$$\begin{cases} \pi_h \left(1 - \sum_{i=0}^{n+1} p_i\right) = a\,\beta_{vh}\,S_h^*\,\dfrac{I_v^*}{N_h} + \mu_h S_h^* \\ (\mu_h + \nu_h + \eta)E_h^* = p_0\pi_h + a\beta_{vh}\,S_h^*\,\dfrac{I_v^*}{N_h} \\ \alpha_1 I_1^* = p_1\pi_h + \nu_h E_h^* + \sum_{j=2}^{n} m_{1j} I_j^* \\ \alpha_2 I_2^* = p_2\pi_h + \sum_{j=1}^{n} m_{2j} I_j^* \\ \vdots \\ \alpha_i I_i^* = p_i\pi_h + \sum_{j=1}^{n} m_{ij} I_j^* \\ \alpha_n I_n^* = p_n\pi_h + \sum_{j=1}^{n} m_{nj} I_j^* \\ \Lambda_v = aS_v^* \sum_{i=1}^{n} \dfrac{\beta_i I_i^*}{N_h} + (\mu_v + \delta_v)S_v^* \\ (\mu_v + \nu_v + \delta_v)E_v^* = aS_v^* \sum_{i=1}^{n} \dfrac{\beta_i I_i^*}{N_h} \\ (\mu_v + \delta_v)I_v^* = \nu_v E_v^* \end{cases} \tag{10}$$

The derivative of $\mathcal{V}_h$ along the trajectories of System (2) is:

$$\begin{aligned} \dot{\mathcal{V}}_h &= c_0\left(1 - \frac{S_h^*}{S_h}\right)\dot{S}_h + c_0\left(1 - \frac{E_h^*}{E_h}\right)\dot{E}_h + \sum_{i=1}^{n} c_i\left(1 - \frac{I_i^*}{I_i}\right)\dot{I}_i \\ &= c_0\mu_h S_h^*\left(2 - \frac{S_h}{S_h^*} - \frac{S_h^*}{S_h}\right) + c_0 a\beta_{vh}S_h^*\frac{I_v^*}{N_h}\left(2 - \frac{S_h^*}{S_h} - \frac{S_h}{S_h^*}\frac{I_v}{I_v^*}\frac{E_h^*}{E_h}\right) \\ &\quad + c_0 p_0\pi\left(2 - \frac{E_h^*}{E_h} - \frac{E_h}{E_h^*}\right) - c_0\left(\beta_{vh}\,S_h^*\frac{I_v^*}{N_h}\right)\frac{E_h}{E_h^*} + c_0 a\,\beta_{vh}S_h^*\frac{I_v}{N_h} \\ &\quad + \sum_{i=1}^{n} c_i\left(1 - \frac{I_i^*}{I_i}\right)\dot{I}_i. \end{aligned} \tag{11}$$

Using the endemic relation $\alpha_1 I_1^* = p_1\pi_h + \nu_h E_h^* + \sum_{j=1}^{n} m_{1j} I_j^*$, and the relationship between c_0 and c_1, Equation (11) yields to

$$\begin{aligned} \dot{\mathcal{V}}_h &= c_0\mu_h S_h^*\left(2 - \frac{S_h}{S_h^*} - \frac{S_h^*}{S_h}\right) + c_0 a\beta_{vh}S_h^*\frac{I_v^*}{N_h}\left(3 - \frac{S_h^*}{S_h} - \frac{S_h}{S_h^*}\frac{I_v}{I_v^*}\frac{E_h^*}{E_h} - \frac{E_h}{E_h^*}\frac{I_1^*}{I_1}\right) \\ &\quad + c_0 p_0\pi\left(2 - \frac{E_h^*}{E_h} - \frac{E_h}{E_h^*}\right) + c_0\,a\,\beta_{vh}S_h^*\frac{I_v}{N_h} + c_1 p_1\pi_h\left(2 - \frac{I_1^*}{I_1} - \frac{I_1}{I_1^*}\right) \\ &\quad - c_1\left(\nu_h E_h^* + \sum_{j=1}^{n} m_{1j} I_j^*\right)\frac{I_1}{I_1^*} + c_1\sum_{j=1}^{n} m_{1j} I_j + c_1\sum_{j=1}^{n} m_{1j} I_j^* \\ &\quad - c_1\frac{I_1^*}{I_1}\left(\sum_{j=1}^{n} m_{1j} I_j\right) + \sum_{i=2}^{n} c_i\left(1 - \frac{I_i^*}{I_i}\right)\dot{I}_i \end{aligned} \tag{12}$$

Noting that, from the endemic relations (10), we have $\alpha_i I_i^* = p_i\pi_h + \sum_{j=1}^n m_{ij} I_j^*$, and thus, the last term of Equation (12) leads to

$$\begin{aligned} c_i\left(1-\frac{I_i^*}{I_i}\right)\dot{I}_i &= c_i p_i \pi_h\left(2-\frac{I_i^*}{I_i}-\frac{I_i}{I_i^*}\right)+c_i\sum_{j=1}^n m_{ij}I_j^*-c_i\left(\sum_{j=1}^n m_{ij}I_j^*\right)\frac{I_i}{I_i^*} \\ &\quad +c_i\sum_{j=1}^n m_{ij}I_j-c_i\frac{I_i^*}{I_i}\left(\sum_{j=1}^n m_{ij}I_j\right) \end{aligned} \tag{13}$$

Moreover, we can check that the derivative of $\mathcal{V}_v$ along the trajectories of System (2) is:

$$\begin{aligned} \dot{\mathcal{V}}_v = c_{v,1}\Bigg(\mathcal{A}_v+\sum_{i=1}^n aS_v^*\frac{\beta_i I_i^*}{N_i}\left(3-\frac{S_v^*}{S_v}-\frac{S_v}{S_v^*}\frac{I_i}{I_i^*}\frac{E_v^*}{E_v}-\frac{E_v I_v^*}{E_v^* I_v}\right) \\ +aS_v^*\sum_{i=1}^n\frac{\beta_i I_i}{N_h}-aS_v^*\sum_{i=1}^n\frac{\beta_i I_i^*}{N_h}\frac{I_v}{I_v^*}\Bigg), \end{aligned} \tag{14}$$

where $\mathcal{A}_v = (\mu_v+\delta_v)S_v^*\left(2-\frac{S_v^*}{S_v}-\frac{S_v}{S_v^*}\right)$. Combining equations (12), (13), and (14), we obtain:

$$\begin{aligned} \dot{\mathcal{V}} &= c_0\mu_h S_h^*\left(2-\frac{S_h}{S_h^*}-\frac{S_h^*}{S_h}\right)+c_0 a\beta_{vh}S_h^*\frac{I_v^*}{N_h}\left(3-\frac{S_h^*}{S_h}-\frac{S_h}{S_h^*}\frac{I_v}{I_v^*}\frac{E_h^*}{E_h}-\frac{E_h}{E_h^*}\frac{I_1^*}{I_1}\right) \\ &\quad +c_0 p_0\pi\left(2-\frac{E_h^*}{E_h}-\frac{E_h}{E_h^*}\right)+c_0 a\,\beta_{vh}S_h^*\frac{I_v}{N_h}+\sum_{i=1}^n c_i p_i\pi_h\left(2-\frac{I_i^*}{I_i}-\frac{I_i}{I_i^*}\right) \\ &\quad -c_1\left(\nu_h E_h^*+\sum_{j=1}^n m_{1j}I_j^*\right)\frac{I_1}{I_1^*}+c_1\sum_{j=1}^n m_{1j}I_j+c_1\sum_{j=1}^n m_{1j}I_j^* \\ &\quad -c_1\frac{I_1^*}{I_1}\left(\sum_{j=1}^n m_{1j}I_j\right)+c_{v,1}\left(+aS_v^*\sum_{i=1}^n\frac{\beta_i I_i}{N_h}-aS_v^*\sum_{i=1}^n\frac{\beta_i I_i^*}{N_h}\frac{I_v}{I_v^*}\right) \\ &\quad +\sum_{i=2}^n\Bigg[c_i\sum_{j=1}^n m_{ij}I_j^*-c_i\left(\sum_{j=1}^n m_{ij}I_j^*\right)\frac{I_i}{I_i^*}+c_i\sum_{j=1}^n m_{ij}I_j \\ &\quad -c_i\frac{I_i^*}{I_i}\left(\sum_{j=1}^n m_{ij}I_j\right)\Bigg]+c_{v,1}\mathcal{A}_v \\ &\quad +c_{v,1}\sum_{i=1}^n aS_v^*\frac{\beta_i I_i^*}{N_i}\left(3-\frac{S_v^*}{S_v}-\frac{S_v}{S_v^*}\frac{I_i}{I_i^*}\frac{E_v^*}{E_v}-\frac{E_v I_v^*}{E_v^* I_v}\right) \end{aligned} \tag{15}$$

Given the relationship (9), the linear terms in I_v in Equation (15) cancel. Furthermore, by substituting $\mathcal{A}_v$ by its expression and $c_{v,1}$ by their expressions, Equation (15) leads to

$$\begin{aligned} \dot{\mathcal{V}} &= c_0\mu_h S_h^*\left(2-\frac{S_h}{S_h^*}-\frac{S_h^*}{S_h}\right)+c_{v,1}(\mu_v+\delta_v)S_v^*\left(2-\frac{S_v^*}{S_v}-\frac{S_v}{S_v^*}\right) \\ &\quad +c_0 p_0\pi\left(2-\frac{E_h^*}{E_h}-\frac{E_h}{E_h^*}\right)+\sum_{i=1}^n c_i p_i\pi_h\left(2-\frac{I_i^*}{I_i}-\frac{I_i}{I_i^*}\right) \end{aligned}$$

$$
\begin{aligned}
&+c_{v,1}\sum_{i=1}^{n} aS_v^*\frac{\beta_i I_i^*}{N_i}\left(6-\frac{S_h^*}{S_h}-\frac{S_h}{S_h^*}\frac{I_v}{I_v^*}\frac{E_h^*}{E_h}-\frac{E_h}{E_h^*}\frac{I_1^*}{I_1}-\frac{S_v^*}{S_v}-\frac{S_v}{S_v^*}\frac{I_i}{I_i^*}\frac{E_v^*}{E_v}-\frac{E_v I_v^*}{E_v^* I_v}\right)\\
&-c_1\left(\nu_h E_h^*+\sum_{j=1}^{n} m_{1j}I_j^*\right)\frac{I_1}{I_1^*}+c_1\sum_{j=1}^{n} m_{1j}I_j+c_1\sum_{j=1}^{n} m_{1j}I_j^*\\
&-c_1\frac{I_1^*}{I_1}\left(\sum_{j=1}^{n} m_{1j}I_j\right)+\sum_{i=2}^{n}\left[c_i\sum_{j=1}^{n} m_{ij}I_j^*-c_i\left(\sum_{j=1}^{n} m_{ij}I_j^*\right)\frac{I_i}{I_i^*}\right.\\
&\left.+c_i\sum_{j=1}^{n} m_{ij}I_j-c_i\frac{I_i^*}{I_i}\left(\sum_{j=1}^{n} m_{ij}I_j\right)\right]+c_1\frac{\nu_h E_h^*}{\sum_{l=1}^{n}\beta_l I_l^*}\left(\sum_{i=1}^{n}\beta_i I_i\right). \qquad (16)
\end{aligned}
$$

We choose the vector $c=(c_1,c_2,\ldots,c_n)^T$ to be the solution of the linear system $Bc=0$, where

$$
B=\begin{pmatrix}
-\diamond_{11} & m_{21}I_1^* & m_{31}I_1^* & \ldots & \ldots & m_{n1}I_1^*\\
\nu_h E_h^*\frac{\beta_2 I_2^*}{\sum_{i=1}^{n}\beta_i I_i^*}+m_{12}I_2^* & -\diamond_{22} & m_{32}I_2^* & \ldots & \ldots & m_{n2}I_2^*\\
\nu_h E_h^*\frac{\beta_3 I_3^*}{\sum_{i=1}^{n}\beta_i I_i^*}+m_{13}I_3^* & m_{23}I_3^* & -\diamond_{33} & \ldots & \ldots & m_{n3}I_n^*\\
\vdots & \vdots & \vdots & \ddots & \ddots & \vdots\\
\nu_h E_h^*\frac{\beta_n I_n^*}{\sum_{i=1}^{n}\beta_i I_i^*}+m_{1n}I_n^* & m_{2n}I_n^* & m_{3n}I_n^* & \ldots & \ldots & -\diamond_{nn}
\end{pmatrix} \qquad (17)
$$

where

$$
\diamond_{11}=\left(\nu_h E_h^*\frac{\sum_{i=2}^{n}\beta_i I_i^*}{\sum_{i=1}^{n}\beta_i I_i^*}+\sum_{j=1}^{n} m_{1j}I_j^*\right),\quad \text{and for } k\geq 2,\quad \diamond_{kk}=\sum_{j=1}^{n} m_{kj}I_j^*.
$$

The matrix B is irreducible. Indeed, since $\mathbf{I}_h^*\gg 0$, we notice that all elements of the second upper diagonal of B are all non zero, as $m_{i+1,i}=\gamma_{i,i+1}$, and thus represent the incremental transition between infectious classes. This, along with the first column, makes the matrix B irreducible. Hence, it could be shown that $\dim(\ker(B))=1$; and by the Kirchhoff's matrix tree theorem[5, 27], $c_i=-C_{ii}\gg 0$ where C_{ii} is the cofactor of the i^{th} diagonal of B. Hence, it exists $c=(c_1,c_2,\ldots,c_n)^T\gg 0$ such that $Bc=0$. Moreover, this implies that, in Equation (16), we have:

$$
\begin{aligned}
0 \;=\; &-c_1\left(\nu_h E_h^*+\sum_{j=1}^{n} m_{1j}I_j^*\right)\frac{I_1}{I_1^*}+c_1\sum_{j=1}^{n} m_{1j}I_j+c_1\sum_{j=1}^{n} m_{1j}I_j^*\\
&+\sum_{i=2}^{n}\left[c_i\sum_{j=1}^{n} m_{ij}I_j^*-c_i\left(\sum_{j=1}^{n} m_{ij}I_j^*\right)\frac{I_i}{I_i^*}+c_i\sum_{j=1}^{n} m_{ij}I_j\right]\\
&+c_1\frac{\nu_h E_h^*}{\sum_{l=1}^{n}\beta_l I_l^*}\left(\sum_{i=1}^{n}\beta_i I_i\right)
\end{aligned}
$$

Thus, (16) yields to:

$$
\begin{aligned}
\dot{\mathcal{V}}=\;&c_0\mu_h S_h^*\left(2-\frac{S_h}{S_h^*}-\frac{S_h^*}{S_h}\right)+c_{v,1}(\mu_v+\delta_v)S_v^*\left(2-\frac{S_v^*}{S_v}-\frac{S_v}{S_v^*}\right)\\
&+c_0p_0\pi\left(2-\frac{E_h^*}{E_h}-\frac{E_h}{E_h^*}\right)+\sum_{i=1}^{n} c_i p_i\pi_h\left(2-\frac{I_i^*}{I_i}-\frac{I_i}{I_i^*}\right)
\end{aligned}
$$

$$+ c_{v,1} \sum_{i=1}^{n} a S_v^* \frac{\beta_i I_i^*}{N_i} \underbrace{\left(6 - \frac{S_h^*}{S_h} - \frac{S_h}{S_h^*}\frac{I_v}{I_v^*}\frac{E_h^*}{E_h} - \frac{E_h}{E_h^*}\frac{I_1^*}{I_1} - \frac{S_v^*}{S_v} - \frac{S_v}{S_v^*}\frac{I_i}{I_i^*}\frac{E_v^*}{E_v} - \frac{E_v I_v^*}{E_v^* I_v}\right)}_{\mathcal{W}_i}$$

$$+ \sum_{i=1}^{n}\sum_{j=1}^{n} c_i m_{ij} I_j^* \left(1 - \frac{I_i^*}{I_i}\frac{I_j^*}{I_j}\right). \tag{18}$$

The first three terms of (18) are definite-positive. Now, we will break down the last two terms in (18) into definite-negative terms. Indeed, following [16], we transform each theses expressions as sums of terms in the form of $f(x) = 1 - x + \ln x$. To this end, we will use the fact that the function $f(x)$ is definite negative around $x^* = 1$. Indeed, using the properties of natural logarithm function, the expression of $\mathcal{W}_i$ in (18) could be written as:

$$\begin{aligned}
\mathcal{W}_i &= 6 - \frac{S_h^*}{S_h} - \frac{S_h}{S_h^*}\frac{I_v}{I_v^*}\frac{E_h^*}{E_h} - \frac{E_h}{E_h^*}\frac{I_1^*}{I_1} - \frac{S_v^*}{S_v} - \frac{S_v}{S_v^*}\frac{I_i}{I_i^*}\frac{E_v^*}{E_v} - \frac{E_v I_v^*}{E_v^* I_v} \\
&= \left(1 - \frac{S_h^*}{S_h} + \ln\frac{S_h^*}{S_h}\right) + \left(1 - \frac{S_h}{S_h^*}\frac{I_v}{I_v^*}\frac{E_h^*}{E_h} + \ln\frac{S_h I_v E_h^*}{S_h^* I_v^* E_h}\right) + \left(1 - \frac{E_v I_v^*}{E_v^* I_v} + \ln\frac{E_v I_v^*}{E_v^* I_v}\right) \\
&+ \left(1 - \frac{E_h}{E_h^*}\frac{I_1^*}{I_1} + \ln\frac{E_h I_1^*}{E_h^* I_1}\right) + \left(1 - \frac{S_v I_i E_v^*}{S_v^* I_i^* E_v} + \ln\frac{S_v I_i E_v^*}{S_v^* I_i^* E_v}\right) + \left(1 - \frac{S_v^*}{S_v} + \ln\frac{S_v^*}{S_v}\right) \\
&+ \ln\frac{I_1}{I_1^*}\frac{I_i^*}{I_i}.
\end{aligned}$$

Noting that

$$1 - \frac{I_i^*}{I_i}\frac{I_j}{I_j^*} = 1 - \frac{I_i^*}{I_i}\frac{I_j}{I_j^*} + \ln\frac{I_i^* I_j}{I_i I_j^*} + \ln\frac{I_i I_j^*}{I_i^* I_j},$$

and substituting the expression of $\mathcal{W}_i$, Equation (18) becomes

$$\begin{aligned}
\dot{\mathcal{V}} &= c_0 \mu_h S_h^* \left(2 - \frac{S_h}{S_h^*} - \frac{S_h^*}{S_h}\right) + c_{v,1}(\mu_v + \delta_v) S_v^* \left(2 - \frac{S_v^*}{S_v} - \frac{S_v}{S_v^*}\right) \\
&+ c_{v,1} a S_v^* \sum_{i=1}^{n} \frac{\beta_i I_i^*}{N_h} \left[\left(1 - \frac{S_h^*}{S_h} + \ln\frac{S_h^*}{S_h}\right) + \left(1 - \frac{S_h}{S_h^*}\frac{I_v}{I_v^*}\frac{E_h^*}{E_h} + \ln\frac{S_h I_v E_h^*}{S_h^* I_v^* E_h}\right)\right. \\
&+ \left(1 - \frac{E_v I_v^*}{E_v^* I_v} + \ln\frac{E_v I_v^*}{E_v^* I_v}\right) + \left(1 - \frac{E_h}{E_h^*}\frac{I_1^*}{I_1} + \ln\frac{E_h I_1^*}{E_h^* I_1}\right) + \left(1 - \frac{S_v I_i E_v^*}{S_v^* I_i^* E_v}\right. \\
&\left.\left. + \ln\frac{S_v I_i E_v^*}{S_v^* I_i^* E_v}\right) + \left(1 - \frac{S_v^*}{S_v} + \ln\frac{S_v^*}{S_v}\right)\right] + c_0 p \pi \left(2 - \frac{E_h^*}{E_h} - \frac{E_h}{E_h^*}\right) \\
&+ \sum_{i=1}^{n} c_i p_i \pi_h \left(2 - \frac{I_i^*}{I_i} - \frac{I_i}{I_i^*}\right) + \sum_{i=1}^{n} c_i \sum_{j=1}^{n} m_{ij} I_j^* \left(1 - \frac{I_i^*}{I_i}\frac{I_j}{I_j^*} + \ln\frac{I_i^* I_j}{I_i I_j^*}\right) \\
&+ \underbrace{c_{v,1} a S_v^* \sum_{i=1}^{n} \frac{\beta_i I_i^*}{N_h} \ln\frac{I_1}{I_1^*}\frac{I_i^*}{I_i} + \sum_{i=1}^{n} c_i \sum_{j=1}^{n} m_{ij} I_j^* \ln\frac{I_i I_j^*}{I_i^* I_j}}_{\mathcal{S}}.
\end{aligned} \tag{19}$$

All but the last two sums in (19) are definite negative. Let us denote by $\mathcal{S}$ the sum of these two sums. We focus on proving that $\mathcal{S} := 0$. Indeed, recall the expression of $c_{v,1}$ in terms of c_1, given in (9):

$$c_{v,1}\frac{a S_v^*}{N_h} = c_1 \frac{\nu_h E_h^*}{\sum_{l=1}^{n} \beta_l I_l^*}.$$

By replacing $c_{v,1}$ by its value in $\mathcal{S}$, we obtain,

$$\begin{aligned}\mathcal{S} &= c_{v,1} a S_v^* \sum_{i=1}^{n} \frac{\beta_i I_i^*}{N_h} \ln \frac{I_1}{I_1^*} \frac{I_i^*}{I_i} + \sum_{i=1}^{n} c_i \sum_{j=1}^{n} m_{ij} I_j^* \ln \frac{I_i I_j^*}{I_i^* I_j} \\ &= c_1 \frac{\nu_h E_h^*}{\sum_{l=1}^{n} \beta_l I_l^*} \sum_{i=1}^{n} \beta_i I_i^* \ln \frac{I_1}{I_1^*} \frac{I_i^*}{I_i} + \sum_{i=1}^{n} c_i \sum_{j=1}^{n} m_{ij} I_j^* \ln \frac{I_i I_j^*}{I_i^* I_j} \\ &= c_1 \sum_{j=1}^{n} \ln \frac{I_1 I_j^*}{I_1^* I_j} \left[\frac{\nu_h E_h^*}{\sum_{l=1}^{n} \beta_l I_l^*} \beta_j I_j^* + m_{1j} I_j^* \right] + \sum_{i=2}^{n} c_i \sum_{j=1}^{n} m_{ij} I_j^* \ln \frac{I_i I_j^*}{I_i^* I_j} \end{aligned} \tag{20}$$

However, since c_i are the components of the solution of $Bc = 0$ where B is given in (17), it follows that, for any $j \geq 2$,

$$c_1 \left(\nu_h E_h^* \frac{\beta_j I_j^*}{\sum_{l=1}^{n} \beta_l I_l^*} + m_{1j} I_j^* \right) = c_j \left(\sum_{k=1}^{n} m_{jk} I_k^* \right) - \sum_{i=2}^{n} c_i m_{ij} I_j^*,$$

Plugging this expression into Equation (20), and using again the properties of natural logarithms, we obtain:

$$\begin{aligned}\mathcal{S} &= \sum_{j=1}^{n} \ln \frac{I_1 I_j^*}{I_1^* I_j} \left[c_j \left(\sum_{k=1}^{n} m_{jk} I_k^* \right) - \sum_{i=2}^{n} c_i m_{ij} I_j^* \right] + \sum_{i=2}^{n} c_i \sum_{j=1}^{n} m_{ij} I_j^* \ln \frac{I_i I_j^*}{I_i^* I_j} \\ &= \sum_{i=1}^{n} c_i \ln \frac{I_1 I_i^*}{I_1^* I_i} \left(\sum_{k=1}^{n} m_{ik} I_k^* \right) + \sum_{i=2}^{n} c_i \sum_{j=1}^{n} m_{ij} I_j^* \left[-\ln \frac{I_1 I_j^*}{I_1^* I_j} + \ln \frac{I_i I_j^*}{I_i^* I_j} \right] \\ &= \sum_{i=2}^{n} c_i \ln \frac{I_1 I_i^*}{I_1^* I_i} \left(\sum_{j=1}^{n} m_{ij} I_j^* \right) + \sum_{i=2}^{n} c_i \sum_{j=1}^{n} m_{ij} I_j^* \left[\ln \frac{I_1^* I_i}{I_1 I_i^*} \right] \\ &:= 0, \end{aligned} \tag{21}$$

since for $i = 1$, the coefficient of the sum is $\ln 1 = 0$. Finally using Equation (19) and Equation (21), the derivative of $\mathcal{V}$ along the trajectories of Equation (2) is

$$\begin{aligned}\dot{\mathcal{V}} &= c_0 \mu_h S_h^* \left(2 - \frac{S_h}{S_h^*} - \frac{S_h^*}{S_h} \right) + c_{v,1} (\mu_v + \delta_v) S_v^* \left(2 - \frac{S_v^*}{S_v} - \frac{S_v}{S_v^*} \right) \\ &+ c_{v,1} a S_v^* \sum_{i=1}^{n} \frac{\beta_i I_i^*}{N_h} \left[\left(1 - \frac{S_h^*}{S_h} + \ln \frac{S_h^*}{S_h} \right) + \left(1 - \frac{S_h}{S_h^*} \frac{I_v}{I_v^*} \frac{E_h^*}{E_h} + \ln \frac{S_h I_v E_h^*}{S_h^* I_v^* E_h} \right) \right. \\ &+ \left(1 - \frac{E_v I_v^*}{E_v^* I_v} + \ln \frac{E_v I_v^*}{E_v^* I_v} \right) + \left(1 - \frac{E_h}{E_h^*} \frac{I_1^*}{I_1} + \ln \frac{E_h I_1^*}{E_h^* I_1} \right) + \left(1 - \frac{S_v I_i E_v^*}{S_v^* I_i^* E_v} \right. \\ &\left. \left. + \ln \frac{S_v I_i E_v^*}{S_v^* I_i^* E_v} \right) + \left(1 - \frac{S_v^*}{S_v} + \ln \frac{S_v^*}{S_v} \right) \right] + c_0 p_0 \pi \left(2 - \frac{E_h^*}{E_h} - \frac{E_h}{E_h^*} \right) \\ &+ \sum_{i=1}^{n} c_i p_i \pi_h \left(2 - \frac{I_i^*}{I_i} - \frac{I_i}{I_i^*} \right) + \sum_{i=1}^{n} c_i \sum_{j=1}^{n} m_{ij} I_j^* \left(1 - \frac{I_i^*}{I_i} \frac{I_j}{I_j^*} + \ln \frac{I_i^* I_j}{I_i I_j^*} \right), \end{aligned} \tag{22}$$

which is definite-negative. Therefore, by Lyapunov's stability theorem, the unique endemic equilibrium is GAS. □

Theorem 3.3. *Let $(S_h^\diamond, 0, \mathbf{I}_h^\diamond, S_v^0, 0, 0)$ be a weakly endemic equilibrium of Model (2). This equilibrium is GAS.*

Proof. Let $(S_h^\diamond, 0, \mathbf{I}_h^\diamond, S_v^0, 0, 0)$ be a weakly endemic equilibrium of Model (2).

• If $\boldsymbol{\beta} = 0$, we remark from the vector's equations in Model (2) that $S_v \to S_v^0 := \frac{\pi_v}{\mu_v+\delta_v}$, $E_v \to 0$ and $I_v \to 0$ as $t \to \infty$. So, by the theory of asymptotically autonomous systems for triangular systems [7, 39], Model (2) is equivalent to

$$\begin{cases} \dot{S}_h = \pi_h \left(1 - \sum_{i=0}^{n+1} p_i\right) - \mu_h S_h \\ \dot{E}_h = p_0 \pi_h - (\mu_h + \nu_h + \eta) E_h \\ \dot{\mathbf{I}}_h = \pi_h \mathbf{p} + \nu_h E_h e_1 - (\operatorname{diag}(\alpha) - M)\mathbf{I}_h \end{cases} \tag{23}$$

System (23) is triangular and linear, and its solutions converge toward $(\bar{S}_h, \bar{E}_h, \bar{\mathbf{I}}_h)$, where $\bar{S}_h := \frac{\Lambda_h}{\mu_h}$, $\bar{E}_h := \frac{p_0 \pi_h}{\mu_h+\nu_h+\eta}$ and $\bar{\mathbf{I}}_h := (\operatorname{diag}(\alpha) - M)^{-1} \left(\pi_h \mathbf{p} + \frac{\nu_h p_0 \pi_h}{\mu_h+\nu_h+\eta} e_1\right)$. Thus, it follows that the weak endemic equilibrium $(\bar{S}_h, \bar{E}_h, \bar{\mathbf{I}}_h, S_v^0, 0, 0)$ of Model (2) is GAS.

Before we start the proof of the next case, let us define the order relation for the vectors as follows: $u \leq v$ if $u_i \leq v_i$, for all i, where u_i and v_i are components of u and v respectively. Similarly, $u < v$ if $u \leq v$ and $u \neq v$. Also $u \gg v$ if $u_i > v_i$, for all i.

• If Item 4 of Theorem 3.1 is satisfied with $\mathcal{N}_0^2(p_0, \mathbf{p}, p_{n+1}) \leq 1$. That is, $\boldsymbol{\beta} \neq 0$, $p_0 = 0$ and $\mathbf{p}$ and M are such that $\left\langle \boldsymbol{\beta} \,\middle|\, (\operatorname{diag}(\alpha) - M)^{-1}\mathbf{p} \right\rangle = 0$. These imply that, using the endemic relations,

$$(\operatorname{diag}(\alpha) - M)^{-1}\mathbf{p} > 0.$$

Moreover, it follows that $\left\langle \boldsymbol{\beta} \,\middle|\, \mathbf{I}_h^\diamond \right\rangle = 0$. This implies that it exists a subset $\mathcal{J}$ of $\{1, 2, \ldots, n\}$ such that $I_i^\diamond = 0$, for all $i \in \mathcal{J}$, $I_i^\diamond > 0$ for $i \in \{1, 2, \ldots, n\} \setminus \mathcal{J}$; and $\beta_i^\diamond > 0$ for $i \in \{1, 2, \ldots, n\} \setminus \mathcal{J}$, and $\beta_i^\diamond = 0$ for $i \in \mathcal{J}$. WLOG, suppose that $\mathcal{J} = \{1, 2, \ldots, s-1\}$ with $s \geq 2$. Hence, the endemic relation $\mathbf{I}_h^\diamond = \pi_h (\operatorname{diag}(\alpha) - M)^{-1}\mathbf{p}$ and the condition $\left\langle \boldsymbol{\beta} \,\middle|\, (\operatorname{diag}(\alpha) - M)^{-1}\mathbf{p} \right\rangle = 0$ imply that M has the form

$$M = \begin{pmatrix} M_{11} & \mathbf{0}_{s-1,n-s+1} \\ M_{21} & M_{22} \end{pmatrix},$$

where $M_{11} \in \mathcal{M}_{s-1,s-1}$, $M_{21} \in \mathcal{M}_{n-s+1,s-1}$, $M_{22} \in \mathcal{M}_{n-s+1,n-s+1}$. Similarly, $p_i = 0$ for all $i \in \mathcal{J}$ and $\mathbf{I}_h^\diamond = (0, \ldots, 0, I_s^\diamond, \ldots, I_n^\diamond)$ where $I_i^\diamond > 0$ for $s \leq i \leq n$.

Let $\mathbf{c} = (\mathbf{c}_1, \mathbf{c}_2)^T$ where $\mathbf{c}_1 = (c_1, \ldots, c_{s-1})^T$ and $\mathbf{c}_2 = (c_s, \ldots, c_n)^T$. The vector $\mathbf{c}_2$ is the solution of $\tilde{B}\mathbf{c}_2 = 0$ where

$$\tilde{B} = \begin{pmatrix} -\tilde{b}_{s,s} & m_{s+1,s} I_s^\diamond & m_{s+2,s} I_s^\diamond & \ldots & \ldots & m_{n,s} I_s^\diamond \\ m_{s,s+1} I_{s+1}^\diamond & -\tilde{b}_{s+1,s+1} & m_{s+2,s+1} I_{s+1}^\diamond & \ldots & \ldots & m_{n,s+1} I_{s+1}^\diamond \\ m_{s,s+2} I_{s+2}^\diamond & m_{s+1,s+2} I_{s+2}^\diamond & -\tilde{b}_{33} & \ldots & \ldots & m_{n,s+2} I_{s+2}^\diamond \\ \vdots & \vdots & \vdots & \ddots & \ddots & \vdots \\ m_{s,n} I_n^\diamond & m_{s+1,n} I_n^\diamond & m_{s+2,n} I_n^\diamond & \ldots & \ldots & -\tilde{b}_{nn} \end{pmatrix},$$

where $\tilde{b}_{kk} = \sum_{j=s}^n m_{kj} I_j^\diamond$ for $s \leq k \leq n$. Since M_{22} is irreducible and $I_i^\diamond > 0$ for all $s \leq i \leq n$, the matrix $\tilde{B}$ is irreducible. Moreover, $\tilde{B}$ is the Laplacian matrix of the graph interconnecting the stages I_i for $s \leq i \leq n$. Hence, as previously stated, Kirchhoff's matrix tree theorem affirms that the solution of $\tilde{B}\mathbf{c}_2 = 0$ is such that $c_i = -C_{ii} \gg 0$, where C_{ii} is the cofactor of i^{th} diagonal element of $\tilde{B}$. Hence $\mathbf{c}_2 \gg 0$.

Let $\mathbf{I}_h^\diamond = (\mathbf{I}_1^\diamond, \mathbf{I}_2^\diamond)^T$ and consider the Lyapunov function candidate $\mathcal{V} = \mathcal{V}_h + \mathcal{V}_v$, where

$$\mathcal{V}_h = c_1 \frac{\nu_h}{\alpha_h} E_h + \langle \mathbf{c}_1 \,|\, \mathbf{I}_1 \rangle + \sum_{i=s}^{n} c_i \int_{I_i^\diamond}^{I_i} \left(1 - \frac{I_i^\diamond}{x}\right) dx, \quad \text{and} \quad \mathcal{V}_v = c_v E_v + c_v \frac{\alpha_v}{\nu_v} I_v,$$

where $c_v = c_1 \frac{\nu_h}{\alpha_h} \frac{a\beta_{vh}\Lambda_h}{\mu_h N_h} \frac{\nu_v}{(\mu_v+\delta_v)\alpha_v}$, $\mathbf{c}_1$ is positive vector to be determined later. The derivative of $\mathcal{V}$ along the trajectories of System (2) is:

$$\begin{aligned}
\dot{\mathcal{V}}_h &= c_1 \frac{\nu_h}{\alpha_h} \dot{E}_h + \langle \mathbf{c}_1 \,|\, \dot{\mathbf{I}}_1^\diamond \rangle + \sum_{i=s}^{n} c_i \left(1 - \frac{I_i^\diamond}{I_i}\right) \dot{I}_i + c_v \dot{E}_v + c_v \frac{\alpha_v}{\nu_v} \dot{I}_v \\
&= c_1 a\, \beta_{vh} \frac{\nu_h}{\alpha_h} \frac{S_h I_v}{N_h} + \langle \mathbf{c}_1 \,|\, (-\mathrm{diag}(\tilde{\alpha}) + M_{11})\mathbf{I}_1 \rangle + \sum_{i=s}^{n} c_i \left(1 - \frac{I_i^\diamond}{I_i}\right) \dot{I}_i, \quad (24)
\end{aligned}$$

where $\tilde{\alpha} = (\alpha_1, \ldots, \alpha_{s-1})$. Moreover, as in the proof of Theorem 3.2, using the fact, for that, for $1 \leq i \leq n$, the c_i are the components of the solution of $\tilde{B}\mathbf{c}_2 = 0$ and

$$\sum_{i=s}^{n} c_i \sum_{j=s}^{n} m_{ij} I_j^\diamond \left(1 - \frac{I_i^\diamond}{I_i}\frac{I_j}{I_j^\diamond}\right) = \sum_{i=s}^{n} c_i \sum_{j=s}^{n} m_{ij} I_j^\diamond \left(1 - \frac{I_i^\diamond}{I_i}\frac{I_j}{I_j^\diamond} + \ln \frac{I_i^\diamond}{I_i}\frac{I_j}{I_j^\diamond}\right),$$

it could be shown that Equation (24) implies that

$$\begin{aligned}
\sum_{i=s}^{n} c_i \left(1 - \frac{I_i^*}{I_i}\right) \dot{I}_i &= \sum_{i=s}^{n} c_i p_i \pi_h \left(2 - \frac{I_i^\diamond}{I_i} - \frac{I_i}{I_i^\diamond}\right) + \sum_{i=s}^{n} c_i \sum_{j=s}^{n} m_{ij} I_j^\diamond \left(1 - \frac{I_i^\diamond}{I_i}\frac{I_j}{I_j^\diamond} \right. \\
&\quad \left. + \ln \frac{I_i^\diamond}{I_i}\frac{I_j}{I_j^\diamond}\right) - \sum_{i=s}^{n} c_i \frac{I_i^\diamond}{I_i} \sum_{i=1}^{s-1} m_{ij} I_j + \sum_{i=s}^{n} c_i \sum_{j=1}^{s-1} m_{ij} I_j \\
&:= \sum_{i=s}^{n} c_i p_i \pi_h \left(2 - \frac{I_i^*}{I_i} - \frac{I_i}{I_i^*}\right) + \sum_{i=s}^{n} c_i \sum_{j=s}^{n} m_{ij} I_j^\diamond \left(1 - \frac{I_i^\diamond}{I_i}\frac{I_j}{I_j^\diamond} \right. \\
&\quad \left. + \ln \frac{I_i^\diamond}{I_i}\frac{I_j}{I_j^\diamond}\right) - \sum_{i=s}^{n} c_i \frac{I_i^\diamond}{I_i} \sum_{i=1}^{s-1} m_{ij} I_j + \mathbf{c}_2^T M_{21} \mathbf{I}_1. \quad (25)
\end{aligned}$$

We choose $\mathbf{c}_1$ to be the solution of $(-\mathrm{diag}(\tilde{\alpha}) + M_{11}^T + \bar{\boldsymbol{\beta}}\tilde{e}_1^T)\mathbf{c}_1 = -M_{21}^T \mathbf{c}_2$, where $\bar{\boldsymbol{\beta}} = \frac{a^2 \beta_{vh}\Lambda_h}{\mu_h N_h} \frac{\nu_v \nu_h}{(\mu_v+\delta_v)\alpha_v \alpha_h} \frac{N_v}{N_h} \tilde{\boldsymbol{\beta}}$, with $\tilde{\boldsymbol{\beta}} = (\beta_1, \ldots, \beta_{s-1})$ and $\tilde{e}_1$ the fist canonical vector of $\mathbb{R}^{s-1}$. This solution exists and $\mathbf{c}_1 \geq 0$ since $\mathbf{c}_2 \gg 0$ and $-(-\mathrm{diag}(\tilde{\alpha}) + M_{11}^T + \bar{\boldsymbol{\beta}}\tilde{e}_1^T)^{-1} \geq 0$ as $-\mathrm{diag}(\tilde{\alpha}) + M_{11}^T + \bar{\boldsymbol{\beta}}\tilde{e}_1^T$ is a Metzler invertible matrix.

Hence, Equations (24) and (25) leads to

$$\begin{aligned}
\dot{\mathcal{V}}_h &= c_1 a\, \beta_{vh} \frac{\nu_h}{\alpha_h} \frac{S_h I_v}{N_h} + \langle \mathbf{c}_1 \,|\, (-\mathrm{diag}(\tilde{\alpha}) + M_{11})\mathbf{I}_1 \rangle + \sum_{i=s}^{n} c_i p_i \pi_h \left(2 - \frac{I_i^\diamond}{I_i} - \frac{I_i}{I_i^\diamond}\right) \\
&\quad + \sum_{i=s}^{n} c_i \sum_{j=s}^{n} m_{ij} I_j^\diamond \left(1 - \frac{I_i^\diamond}{I_i}\frac{I_j}{I_j^\diamond} + \ln \frac{I_i^\diamond}{I_i}\frac{I_j}{I_j^\diamond}\right) - \sum_{i=s}^{n} c_i \frac{I_i^\diamond}{I_i} \sum_{i=1}^{s-1} m_{ij} I_j \\
&\quad + \mathbf{c}_2^T M_{21} \mathbf{I}_1. \quad (26)
\end{aligned}$$

However,

$$\begin{aligned}\left\langle \mathbf{c}_1 \,\middle|\, (-\mathrm{diag}(\tilde{\alpha}) + M_{11})\mathbf{I}_1 \right\rangle + \mathbf{c}_2^T M_{21}\mathbf{I}_1 &= \left\langle (-\mathrm{diag}(\tilde{\alpha}) + M_{11}^T)\mathbf{c}_1 + M_{21}^T\mathbf{c}_2 \,\middle|\, \mathbf{I}_1 \right\rangle \\ &= -\left\langle \bar{\boldsymbol{\beta}}\tilde{e}_1^T\mathbf{c}_1 \,\middle|\, \mathbf{I}_1 \right\rangle \\ &:= -c_1\frac{a^2\beta_{vh}\Lambda_h N_v}{\mu_h N_h^2}\frac{\nu_v\nu_h}{(\mu_v+\delta_v)\alpha_v\alpha_h}\left\langle \tilde{\boldsymbol{\beta}} \,\middle|\, \mathbf{I}_1 \right\rangle.\end{aligned}$$

Hence, Equation (26) leads to

$$\begin{aligned}\dot{\mathcal{V}}_h =& c_1 a\,\beta_{vh}\frac{\nu_h}{\alpha_h}\frac{S_h I_v}{N_h} + \sum_{i=s}^{n} c_i p_i \pi_h \left(2 - \frac{I_i^\diamond}{I_i} - \frac{I_i}{I_i^\diamond}\right) - c_1\frac{a^2\beta_{vh}\Lambda_h N_v}{\mu_h N_h^2}\frac{\nu_v\nu_h\left\langle \tilde{\boldsymbol{\beta}} \,\middle|\, \mathbf{I}_1 \right\rangle}{(\mu_v+\delta_v)\alpha_v\alpha_h} \\ &+ \sum_{i=s}^{n} c_i \sum_{j=s}^{n} m_{ij} I_j^\diamond \left(1 - \frac{I_i^\diamond}{I_i}\frac{I_j}{I_j^\diamond} + \ln\frac{I_i^\diamond}{I_i}\frac{I_j}{I_j^\diamond}\right) - \sum_{i=s}^{n} c_i \frac{I_i^\diamond}{I_i}\sum_{i=1}^{s-1} m_{ij} I_j. \qquad (27)\end{aligned}$$

We can check that derivative of $\mathcal{V}_v$ along the trajectories of (2)

$$\begin{aligned}\dot{\mathcal{V}}_v &= c_v\dot{E}_v + c_v\frac{\alpha_v}{\nu_v}\dot{I}_v \\ &= c_v\left(a\frac{S_v}{N_h}\left\langle \boldsymbol{\beta} \,\middle|\, \mathbf{I}_h \right\rangle - \alpha_v E_v\right) + c_v\frac{\alpha_v}{\nu_v}\left(\nu_v E_v - (\mu_v+\delta_v)I_v\right) \\ &= c_1 a^2\frac{\beta_{vh}\Lambda_h}{\mu_h N_h}\frac{\nu_v\nu_h}{(\mu_v+\delta_v)\alpha_v\alpha_h}\frac{S_v}{N_h}\left\langle \boldsymbol{\beta} \,\middle|\, \mathbf{I}_h \right\rangle - c_1\frac{\nu_h}{\alpha_h}\frac{a\beta_{vh}\Lambda_h}{\mu_h N_h}I_v \\ &= c_1 a^2\frac{\beta_{vh}\Lambda_h}{\mu_h N_h}\frac{\nu_v\nu_h}{(\mu_v+\delta_v)\alpha_v\alpha_h}\frac{S_v}{N_h}\left\langle \tilde{\boldsymbol{\beta}} \,\middle|\, \mathbf{I}_1 \right\rangle - c_1\frac{\nu_h}{\alpha_h}\frac{a\beta_{vh}\Lambda_h}{\mu_h N_h}I_v, \qquad (28)\end{aligned}$$

since $\left\langle \boldsymbol{\beta} \,\middle|\, \mathbf{I}_h \right\rangle = \left\langle \tilde{\boldsymbol{\beta}} \,\middle|\, \mathbf{I}_1 \right\rangle$. Finally, the derivative of $\mathcal{V} = \mathcal{V}_h + \mathcal{V}_v$ along the trajectories of (2) is obtained by combining Equation (27) and Equation (28) as follows:

$$\begin{aligned}\dot{\mathcal{V}} &= c_1 a\,\beta_{vh}\frac{\nu_h}{\alpha_h}\frac{1}{N_h}\left(S_h - \frac{\Lambda_h}{\mu_h}\right)I_v - c_1\frac{a^2\beta_{vh}\Lambda_h}{\mu_h N_h}\frac{\nu_v\nu_h}{(\mu_v+\delta_v)\alpha_v\alpha_h}\frac{S_v - N_v}{N_h}\left\langle \tilde{\boldsymbol{\beta}} \,\middle|\, \mathbf{I}_1 \right\rangle \\ &+ \sum_{i=s}^{n} c_i p_i \pi_h \left(2 - \frac{I_i^\diamond}{I_i} - \frac{I_i}{I_i^\diamond}\right) + \sum_{i=s}^{n} c_i \sum_{j=s}^{n} m_{ij} I_j^\diamond \left(1 - \frac{I_i^\diamond}{I_i}\frac{I_j}{I_j^\diamond} + \ln\frac{I_i^\diamond}{I_i}\frac{I_j}{I_j^\diamond}\right) \\ &- \sum_{i=s}^{n} c_i \frac{I_i^\diamond}{I_i}\sum_{i=1}^{s-1} m_{ij} I_j.\end{aligned}$$

Moreover, using the equation of $\dot{S}_h$ and $\dot{S}_v$ in Model (2), it is straightforward that $S_h \le \frac{\Lambda_h}{\mu_h}$ and $S_v \le N_v := \frac{\pi_v}{\mu_v+\delta_v}$, where $\Lambda_h = \pi_h\left(1 - \sum_{i=0}^{n+1} p_i\right)$. Hence $\dot{\mathcal{V}} \le 0$. Therefore, by Lyapunov's theorem this proves the stability of the weakly endemic equilibrium $(S_h^\diamond, 0, \mathbf{I}_h^\diamond, S_v^0, 0, 0)$. Furthermore, $\dot{\mathcal{V}}$ is the sum of five nonpositive terms, of which two are definite-negative. Hence, it is straightforward that the largest invariant set on which $\dot{\mathcal{V}} = 0$ is reduced to $(S_h^\diamond, 0, \mathbf{I}_h^\diamond, S_v^0, 0, 0)$. Thus, by LaSalle's principle, $(S_h^\diamond, 0, \mathbf{I}_h^\diamond, S_v^0, 0, 0)$ is asymptotically stable. This completes the proof of the global asymptotic stability of the weakly endemic equilibrium $(S_h^\diamond, 0, \mathbf{I}_h^\diamond, S_v^0, 0, 0)$. □

Per Theorem 3.1, Item 4, a necessary condition to break the host-vector transmission, that is, to maintain the vectors disease-free, is $p = 0$ and $\left\langle \boldsymbol{\beta} \,\middle|\, (\mathrm{diag}(\alpha) - M)^{-1}\mathbf{p} \right\rangle = 0$. The later quantity has an epidemiological interpretation. Indeed, it

means that: a.) there is an influx of infected individuals only to a subset of indices and that the hosts in these stages are unable to infect the vectors and b.) the infectious hosts at these stages do not "ameliorate" their infectiosity to stages in the complement of the subset in which they belong. That is, $\delta_{ij}=0$ for all $i\in A$ and $j\in\{1,2,\dots,n\}\setminus A$, with $p_j>0$ for all $j\in A$ and $p_j=0$ otherwise. In this case, the threshold $\mathcal{N}_0^2(p_0,\mathbf{p},p_{n+1})$ determine whether or not the vector populations become disease-free. If $\mathcal{N}_0^2(p_0,\mathbf{p},p_{n+1})<1$, the disease dies out in the vector population and it thus, the infectious hosts are contained only into the classes in which they are replenished. This threshold captures the capacity of hosts in stage A to maintain the disease in the vector population. Indeed, we can show that:

$$\begin{aligned}\mathcal{N}_0^2(p_0,\mathbf{p},p_{n+1}) &= \frac{a^2\beta_{vh}\nu_v\nu_h N_v}{\alpha_v(\mu_v+\delta_v)\alpha_h\mu_h}\frac{\pi_h\left(1-\sum_{i=0}^{n+1}p_i\right)}{N_h^2}\left\langle\boldsymbol{\beta}\,\middle|\,(\mathrm{diag}(\alpha)-M)^{-1}e_1\right\rangle\\ &:= \frac{a^2\beta_{vh}\nu_v\nu_h N_v}{\alpha_v(\mu_v+\delta_v)\alpha_h\mu_h}\frac{\pi_h\left(1-\sum_{i=0}^{n+1}p_i\right)}{N_h^2}\left\langle\tilde{\boldsymbol{\beta}}\,\middle|\,(\mathrm{diag}(\tilde{\alpha})-M_{11})^{-1}e_1\right\rangle\end{aligned}$$

In the light of Theorem 3.1, Item 4; Theorem 3.2, and Theorem 3.3, to break the host-vector chain of transmission when there is an influx of infectious hosts into a naïve population and competent vector, a necessary and sufficient condition is $p_0=0$, the vectors $\boldsymbol{\beta}$, $\mathbf{p}$; and the transition matrix M are such that $\left\langle\boldsymbol{\beta}\,\middle|\,(\mathrm{diag}(\alpha)-M)^{-1}\mathbf{p}\right\rangle=0$ and $\mathcal{N}_0^2(p_0,\mathbf{p},p_{n+1})\le 1$, thereby providing for a positive answer to our initial claim.

3.1. **Sharp threshold property.** In this subsection, we investigate the dynamics of Model (2) when $p=p_1=\cdots=p_n=0$. In this case, we obtain the model

$$\begin{cases}\dot{S}_h=\pi_h-a\,\beta_{vh}\,S_h\,\dfrac{I_v}{N_h}-\mu_h S_h\\ \dot{E}_h=a\,\beta_{vh}\,S_h\,\dfrac{I_v}{N_h}-(\mu_h+\nu_h+\eta)E_h\\ \dot{\mathbf{I}}_h=\nu_h E_h e_1-(\mathrm{diag}(\alpha)-M)\mathbf{I}_h\\ \dot{S}_v=\Lambda_v-a\dfrac{S_v}{N_h}\left\langle\boldsymbol{\beta}^T\,\middle|\,\mathbf{I}_h\right\rangle-(\mu_v+\delta_v)S_v\\ \dot{E}_v=a\dfrac{S_v}{N_h}\left\langle\boldsymbol{\beta}^T\,\middle|\,\mathbf{I}_h\right\rangle-(\mu_v+\nu_v+\delta_v)E_v\\ \dot{I}_v=\nu_v E_v-(\mu_v+\delta_v)I_v\end{cases}\tag{29}$$

For the same reason evoked in Section 2, the solutions of System (29) stay positive and bounded. Unlike in Model (2), the Model (29) has a disease free equilibrium (DFE), and is given by $(S_h^0,0,0,S_v^0,0,0)$ with $S_h^0=\frac{\pi_h}{\mu_h}$ and $S_v^0=\frac{\pi_v}{\mu_v+\delta_v}$.

The basic reproduction number $\mathcal{R}_0^2$ is derived using the next generation method. An explicit expression of it is given by

$$\begin{aligned}\mathcal{R}_0^2 &= \frac{a^2\beta_{vh}\nu_h\nu_v N_v}{(\mu_h+\nu_h+\eta)(\nu_v+\mu_v+\delta_v)(\nu_v+\delta_v)N_h}\boldsymbol{\beta}^T(\mathrm{diag}(\alpha)-M)^{-1}e_1\\ &:= \mathcal{N}_0^2(0,\mathbf{0},0).\end{aligned}$$

Note that since the matrix is M is Metzler (off-diagonal elements are non-negative) and invertible, we have $-M^{-1}\ge 0$. Thus, $\mathcal{R}_0^2\ge 0$. The following theorem gives the complete asymptotic behavior of Model (29).

Theorem 3.4. *1. If $\mathcal{R}_0^2 \leq 1$, the DFE is globally asymptotically stable.*
2. If $\mathcal{R}_0^2 > 1$, the DFE is unstable and a unique endemic equilibrium exists and is GAS.

The proof of the first part of Theorem 3.4 follows using, for example, a left-eigenvector argument. We omit the details. The second part is particular case of Theorem 3.2. This result is new in itself.

4. **Illustrations and simulations.** In this section, we provide illustrations to highlight the effects of influx of immigrants and the transfer matrix on the disease dynamics and provide some numerical simulations to showcase the results of Section 3. To do so, we consider the case $n = 4$. That is, there are four infectious stages in the host's infectivity. Unless otherwise stated, we consider the following baseline parameters:

$$\pi_h = 1000, a = 0.7, \beta_{vh} = 0.3, \mu_h = \frac{1}{75 \times 365} \text{ days}^{-1}, \ \nu_h = \frac{1}{15} \text{ days}^{-1},$$
$$\gamma_{12} = \frac{1}{8} \text{ days}^{-1}, \ \gamma_{23} = \gamma_{34} = \frac{1}{6} \text{ days}^{-1}, \ \frac{1}{\eta} = 0 \text{ days}^{-1}, \ \eta_1 = \frac{1}{50} \text{ days}^{-1},$$
$$\eta_2 = \eta_3 = \frac{1}{30} \text{ days}^{-1}, \ \eta_4 = \frac{1}{40} \text{ days}^{-1},$$
$$\pi_v = 10000, \mu_v = \frac{1}{15} \text{ days}^{-1}, \ \nu_v = \frac{1}{4} \text{ days}^{-1}, \ \delta_v = \frac{1}{20} \text{ days}^{-1}.$$

It is worthwhile noting that, although reasonable, these values do not necessarily match any particular arbovirus diseases. We have chosen them to encompass results of Section 3. The transfer matrix M and the vector proportions of influx of infected $\mathbf{p}$ are given by

$$M = \begin{pmatrix} 0 & \delta_{21} & \delta_{31} & \delta_{41} \\ \gamma_{12} & 0 & \delta_{32} & \delta_{42} \\ \gamma_{13} & \gamma_{23} & 0 & \delta_{43} \\ \gamma_{14} & \gamma_{24} & \gamma_{34} & 0 \end{pmatrix}, \quad \mathbf{p} = \begin{pmatrix} p_1 \\ p_2 \\ p_3 \\ p_4 \end{pmatrix}.$$

We vary the parameter p, the vector $\mathbf{p}$ and the matrix M to investigate their impacts on the disease dynamics.

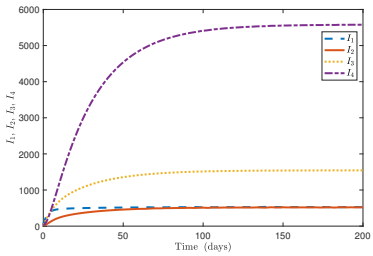
Figure 2(a) and Figure 2(b) depict the dynamics of the Model (2) when there is no transmission form hosts to vectors. That is, whenever $\boldsymbol{\beta} = \mathbf{0}_{\mathbb{R}^n}$. In this case, with $\mathbf{p} \neq \mathbf{0}_{\mathbb{R}^n}$, the infected hosts reach an endemic level (Figure 2(a)) while the disease dies out in the vector population (Figure 2(b)). This is in accordance is the prediction of Theorem 3.1, Item 1, where the weakly endemic equilibrium is GAS (Theorem 3.2).

For $\boldsymbol{\beta} = (0.2, 0, 0, 0.5)^T \neq \mathbf{0}_{\mathbb{R}^4}$ and $p_0 = 0.01$, the trajectories converge to a strongly endemic equilibrium (Figure 2(c) and Figure 2(d)) as the hypotheses of Theorem 3.1, Item 2 are satisfied.

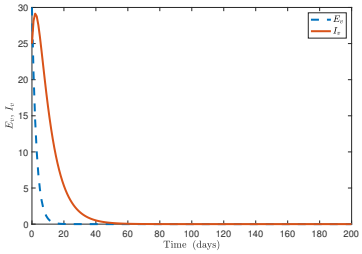
To illustrate Theorem 3.1, Item 3, suppose that $\boldsymbol{\beta} = (\beta_1, 0, 0, 0)^T$ and $\mathbf{p} = (0, 0, p_3, p_4)^T$ where $\beta_1 > 0$, $p_3 > 0$ and $p_4 > 0$. By choosing $\gamma_{14} = \gamma_{24} = \delta_{21} = \delta_{31} = \delta_{42} = 0$, we obtain:

$$\boldsymbol{\beta}^T (\text{diag}(\alpha) - M)^{-1} \mathbf{p} = \frac{\beta_1 \alpha_2 \delta_{41} (p_3 \gamma_{34} + p_4 \alpha_3)}{\det(\text{diag}(\alpha) - M))} > 0. \tag{30}$$

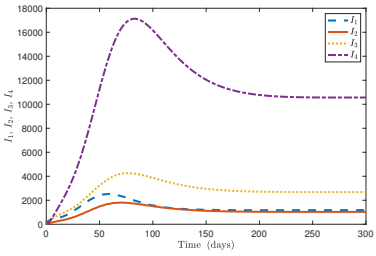
Using this setup, Item 3 of Theorem 3.1 anticipates the existence of an strongly endemic equilibrium. Indeed, Figure 3 represents the dynamics of hosts (Figure 3(a)) and vectors (Figure 3(b)) in Model (2) in this case.



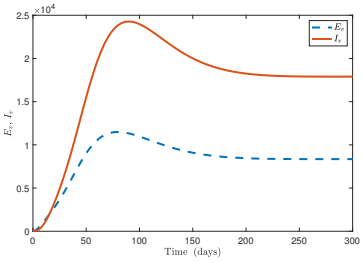
(a) Dynamics of infectious hosts I_i, for $i = 1, \ldots, 4$ when $\boldsymbol{\beta} = \mathbf{0}_{\mathbb{R}^n}$.



(b) Dynamics of infected vectors when $\boldsymbol{\beta} = \mathbf{0}_{\mathbb{R}^n}$.

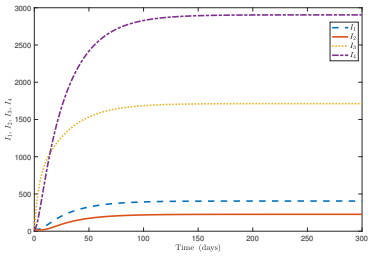


(c) Dynamics of infected hosts when $\boldsymbol{\beta} \neq \mathbf{0}_{\mathbb{R}^4}$ and $p_0 = 0.01 \neq 0$

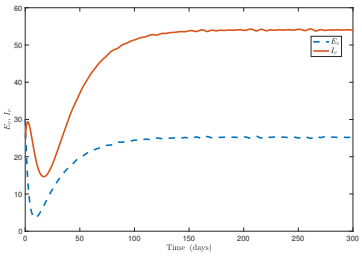


(d) Dynamics of infected vectors when $\boldsymbol{\beta} \neq \mathbf{0}_{\mathbb{R}^n}$ and $p_0 = 0.01 \neq 0$.

FIGURE 2. Effects of host-vector transmission on the dynamics of Model (2) with $n = 4$. The proportions of infectious influx are $p_1 = 0.2$, $p_3 = 0.1$, $p_4 = 0$ and $p_5 = 0.3$. The transfer matrix M is such as $\gamma_{13} = \gamma_{24} = 0.1$, $\gamma_{14} = 0.2$, $\delta_{21} = 0.01$, $\delta_{31} = 0.02$, $\delta_{41} = 0.001$, $\delta_{32} = 0.03$, $\delta_{42} = 0.01$ and $\delta_{43} = 0.03$.



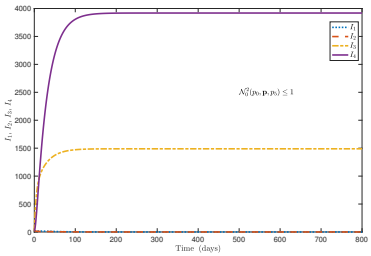
(a) Dynamics of infectious hosts I_i, for $i = 1, \ldots, 4$.



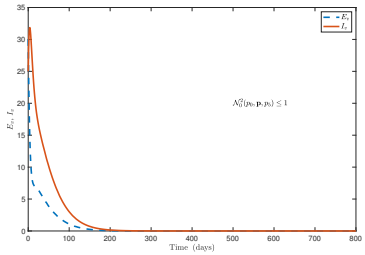
(b) Dynamics of infected vectors.

FIGURE 3. Dynamics of infected hosts and vectors when the hypotheses of Theorem 3.1, Item 3 are satisfied. The proportions of infectious influx are $p_0 = 0$, $\mathbf{p} = (0, 0, p_3, p_4)^T = (0, 0, 0.2, 0.0001)^T$ and $p_5 = 0.3$. The transfer matrix M is such as $\gamma_{13} = 0.1$, $\gamma_{14} = \gamma_{24} = 0$, $\delta_{21} = 0.01$, $\delta_{31} = \delta_{32} = \delta_{42} = 0$, $\delta_{41} = 0.035$, and $\delta_{43} = 0.03$.

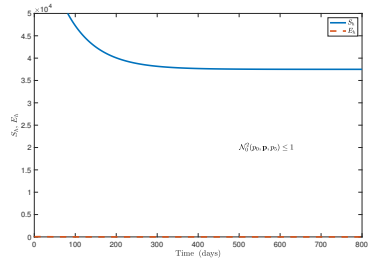
By choosing $\delta_{41} = 0$, Equation (30) implies that $\boldsymbol{\beta}^T(\text{diag}(\alpha) - M)^{-1}\mathbf{p} = 0$ and thus satisfying the conditions of Theorem 3.1, Item 4. And so, a weakly endemic equilibrium $(S_h^\diamond, 0, \mathbf{I}_h^\diamond, S_v^0, 0, 0)$ or a strongly endemic equilibrium $(\tilde{S}_h, \tilde{E}_h, \tilde{\mathbf{I}}_h, \tilde{S}_v, \tilde{E}_v, \tilde{I}_v)$ exists depending on whether $\mathcal{N}_0^2(p_0, \mathbf{p}, p_{n+1})$ is below or greater than unity, respectively. Figure 4(a) shows that the hosts' infection dies out at stage 1 and 2 while it persists at stage 3 and 4. The disease dies out the vectors' population (Figure 4(b)). It is worthwhile noting that the disease is maintained at stages 1 and 2, due to the influx of infectious individuals at these stages, without whom, the interaction between hosts and vectors is not sufficient to sustain the infectious. That is, $\mathcal{N}_0^2(p_0, \mathbf{p}, p_{n+1}) \leq 1$. Under the same transfer matrix M and the infectious influx $\mathbf{p}$ configurations, but choosing the entomological parameters $a = 0.9$ and $\beta_{vh} = 0.9$, we obtain $\mathcal{N}_0^2(p_0, \mathbf{p}, p_{n+1}) = 1.6051 > 1$. This leads to a strongly endemic equilibrium (Figure 5(a) and Figure 5(b)).



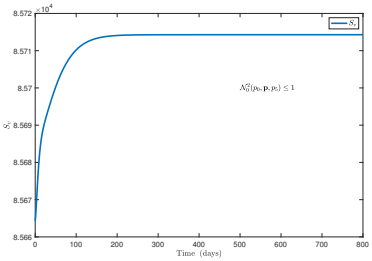
(a) Dynamics of infectious hosts I_i, for $i = 1, \ldots, 4$.



(b) Dynamics of infected and infectious vectors.

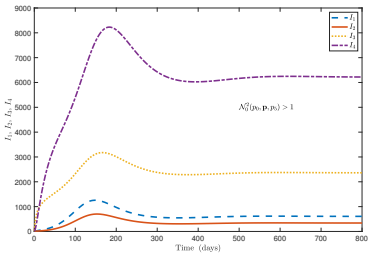


(c) Dynamics of susceptible and latent hosts.

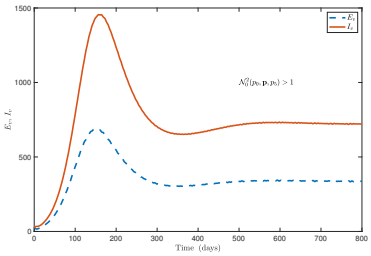


(d) Dynamics of susceptible vectors.

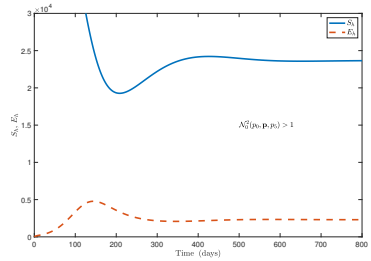
FIGURE 4. Dynamics of infected hosts and vectors when the hypotheses of Theorem 3.1, Item 4 are satisfied. The proportions of infectious influx are $p_0 = 0$, $\mathbf{p} = (0, 0, p_3, p_4)^T = (0, 0, 0.2, 0.0001)^T$ and $p_5 = 0.3$. The transfer matrix M is such as $\gamma_{13} = 0.1$, $\gamma_{14} = \gamma_{24} = 0$, $\delta_{21} = 0.01$, $\delta_{31} = \delta_{32} = \delta_{41} = \delta_{42} = 0$, and $\delta_{43} = 0.03$. With these parameters, $\mathcal{N}_0^2 = 0.3237 \leq 1$. As expected, the vector population will be disease-free (Figure 4(b) and Figure 4(d)) and the infectious hosts are generated only through influx of infectious immigrants at stage 3 and 4 (Figure 4(a) and Figure 4(c)).



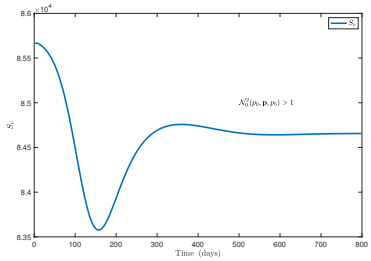
(a) Dynamics of infectious hosts I_i, for $i = 1, \ldots, 4$ when $\mathcal{N}_0^2 > 1$



(b) Dynamics of infected vectors when $\mathcal{N}_0^2 > 1$.



(c) Susceptible and latent hosts when $\mathcal{N}_0^2 > 1$



(d) Dynamics of infected vectors when $\mathcal{N}_0^2 > 1$.

FIGURE 5. Dynamics of infected hosts and vectors when the hypotheses of Theorem 3.1, Item 4 are satisfied. The proportions of infectious influx are $p_0 = 0$, $\mathbf{p} = (0, 0, p_3, p_4)^T = (0, 0, 0.2, 0.0001)^T$ and $p_5 = 0.3$. The transfer matrix M is such as $\gamma_{13} = 0.1$, $\gamma_{14} = \gamma_{24} = 0$, $\delta_{21} = 0.01$, $\delta_{31} = \delta_{32} = \delta_{41} = \delta_{42} = 0$, and $\delta_{43} = 0.03$. Using the values $a = 0.9$ and $\beta_{vh} = 0.9$, $\mathcal{N}_0^2 = 1.6051 > 1$, and thus the trajectories of the system converge towards an interior equilibrium.

5. **Conclusion.** Modeling the dynamics of vector-borne diseases have often been based on the assumption that the recruitment into the population is completely susceptible, and thereby making it difficult to assess the effects of the infected or infectious individuals who enters the population. However, the recent surge of vector-borne diseases such as Chikunguyna and Dengue in areas previously free from the pre-cited diseases, that also coincides with an increase of global travel across the world, makes the study of the effects of new arrivals on vector-borne diseases dynamics a necessity. Indeed, the arrival of new individuals from endemic areas, or the return of local residents after a stint in areas where the vector-borne diseases are endemic, could potentially result in infecting the local vector populations and the cycle of host-vector infection could start or accelerate.

In this paper, we formulate a general staged-progression and stage-regression vector-borne diseases to capture some key features of their dynamics. Particularly, we investigate the effects of the, often swept under the rug, influx of viremic individuals into the hosts and vectors' population dynamics. We also explore the impacts of treatment and repeated exposure. Indeed, assuming the infectious individuals in the population are undergoing a treatment program, whereby improving

their health status; this could lead an infectious individual to go from stage i to a "lower" stage k, where $1 \leq k \leq i$. Similarly, the repeated exposure of infected hosts to infected vectors could lead to more infectious bite. This could lead to an increase of infected and infectious hosts' level of parasitemia and thus worsening its health status. In this case, the infected host progresses from stage i to an "upper" stage k where $1 \leq i \leq k$. And so, we incorporate of these two phenomena of progression and regression on the hosts' dynamics, which happens to have an altering effects on the qualitative dynamics of the model.

We derive a class of vector-borne model with n infectious stages. The host-vector dynamics follows an $SEI^nR - SEI$ framework. We assume that a proportion – of the overall recruitment – p_0 and p_i, for $i = 1, 2, \ldots, n$, of latent and infectious at stage i, respectively, enter into the population. An infectious host at stage i could improve its status from stage i to j, with $j \leq i$, at a rate δ_{ij} or worsen its viremicity from stage i to stage k, with $k \geq i$, at a rate γ_{ik}. We derived all steady states of the general system and provided conditions under which they exist (Theorem 3.1). It turns out that the model has multiple equilibria, depending on the connectivity configuration between host's infectious stages and the influx of infectious arrivals. However, all of the equilibria are either strongly endemic (SEE) – for which all of the infected and infectious components are positive –, or weakly endemic (WEE) – for which some of host and vectors' infected or infectious classes are zero. We show that the influx of latent individuals into the population guarantees the existence of an SEE, and we prove the global asymptotically stability of all equilibria whenever they exist (Theorem 3.2 and Theorem 3.3).

An important particular case is when there is no influx of latent individuals ($p_0 = 0$) but the host-vector transmission vector $\boldsymbol{\beta}$, the proportion of influx of infectious $\mathbf{p}$ and the transfer rates matrix M are such that $\boldsymbol{\beta}^T(\mathrm{diag}(\alpha) - M)^{-1}\mathbf{p} = 0$. In fact, if these conditions are satisfied, it is possible to break the host-vector transmission cycle. Moreover, these conditions have a biological interpretation. Indeed, it means that: a) there is no latent influx and b) there is an influx of infectious hosts only at some stages of infection and the hosts at these stages neither infect the vectors nor they "ameliorate" or "deteriorate" to stages that infect the vector population. This later condition is captured by $\boldsymbol{\beta}^T(\mathrm{diag}(\alpha) - M)^{-1}\mathbf{p} = 0$. More particularly, if these conditions are satisfied, we show that the dynamics of the disease is determined by the threshold $\mathcal{N}_0^2(p_0, \mathbf{p}, p_{n+1})$. The disease will die out in the vector population if $\mathcal{N}_0^2(p_0, \mathbf{p}, p_{n+1})$ is below unity and persists otherwise. In summary, it is possible to break the host-vector chain of transmission when there is an influx of infectious hosts into a naïve population and competent vector if, and only if $p_0 = 0$, $\boldsymbol{\beta}$, $\mathbf{p}$ and M are such that $\boldsymbol{\beta}^T(\mathrm{diag}(\alpha) - M)^{-1}\mathbf{p} = 0$.

Our results show that when there is no influx of infected and infectious individuals, the considered model becomes a vector-borne disease with n infectious stages that accounts for amelioration from and progression to any stages. We show that this model has a sharp threshold phenomenon, for which the dynamics is completely determined by the basic reproduction number $\mathcal{R}_0^2$ (Theorem 3.4). It turns out that $\mathcal{R}_0^2 = \mathcal{N}_0^2(0, \mathbf{0}, 0)$, and if $\mathcal{R}_0^2 \leq 1$, the disease-free equilibrium exists and is globally asymptotically stable. Moreover, if $\mathcal{R}_0^2 > 1$, we show that an endemic equilibrium exists and is globally asymptotically stable.

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